

## RESULT 4

```
US-10-311-034-7
; Sequence 7, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YOE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKI, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Darniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/213,467; 60/215,651; 60/216,605; 60/218,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1
US-10-311-034-7

Query Match 99.5%; Score 2589; DB 15; Length 497;
Best Local Similarity 99.6%; Pred. No. 1.8e-183;
Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAEPIANRSLNLFPGKPEPMTQQOMSPLSREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAEPIANRSLNLFPGKPEPMTQQOMSPLSREGILDALFVLFE 60
Qy 61 ECSQPALMKIKHVSFNVRKYSPTIAELQELQPSAKDFEVSILVGGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSFNVRKYSPTIAELQELQPSAKDFEVSILVGGHFAEVQVVRKATG 120
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## RESULT 5

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US-10-262-511-4
; Sequence 4, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jinfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytex, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zernitsen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pina, Carol E. A.
; APPLICANT: Shency, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Hochenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
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Qy 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLOVAFQDKNHLVLMVEYQPGG 180
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPQLOVAFQDKNHLVLMVEYQPGG 180
Qy 181 DLLSLNRYEDOLDENLIQFYLAELILAVSHVHLNGYVHRDIKPNILVDRFGHIKLVDF 240
Db 181 DLLSLNRYEDOLDENLIQFYLAELILAVSHVHLNGYVHRDIKPNILVDRFGHIKLVDF 240
Qy 241 GSAAKXNSNKNVNAKLPICTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAIEMIXGR 300
Db 241 GSAAKXNSNKNVNAKLPICTPDYMAPEVLTVMNGDGKGTGGLDCDWSVGVIAIEMIXGR 300
Qy 301 SPFAECTSARTFNNTINFORFLKFPDDPKVSSDFDLQSLILCGQKERLKFGLCHPFF 360
Db 301 SPFAECTSARTFNNTINFORFLKFPDDPKVSSDFDLQSLILCGQKERLKFGLCHPFF 360
Qy 361 SKIDWNINRSPPPFVPTLTKSDDDTSNFDPEKSNVSSPQOLSPSGSGELPFVGS 420
Db 361 SKIDWNINRSPPPFVPTLTKSDDDTSNFDPEKSNVSSPQOLSPSGSGELPFVGS 420
Qy 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
Db 421 YSKALGILGRSESVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480
Qy 481 ILPSVYAKGSARGCWL 497
Db 481 ILPSVYAKGSARGCWL 497
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 Db 721 GATTTTGGATGCGCGGAAATGAATCAACAGATGTTGAATGCAAACTCCCGATT 780  
 Qy 781 GGGACCCAGATTACATGCTCCTCAAGTGTGACTGTGATGAGCGGGATGGAAGGC 840  
 Db 781 GGGACCCAGATTACATGCTCCTCAAGTGTGACTGTGATGAGCGGGATGGAAGGC 840  
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 Db 1021 CAAGCTTTGTTGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
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 Db 1201 TCTCTCCGTCGAGCTGAGCCCTCAGGCTTCTCGGTCAGAGAGAGAGAGAGAGAGAG 1260  
 Qy 1261 TTTTCGTACAGCAGAGCAGCTGGGATTCCTTGGTAGATCTGAGTCTGTTGTCGGTCTG 1320  
 Db 1261 TTTTCGTACAGCAGAGCAGCTGGGATTCCTTGGTAGATCTGAGTCTGTTGTCGGTCTG 1320  
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 Db 1321 GACTCCCTCCGAGACTAGCTCAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGTA 1380  
 Qy 1381 CAAGACTCTCAGTA 1440  
 Db 1381 CAAGACTCTCAGTA 1440  
 Qy 1441 TCCAGGATCTCCCGTCCGATATGCAAGGGATCCCGCGGCGGCTGCTGCTCTGA 1500  
 Db 1441 TCCAGGATCTCCCGTCCGATATGCAAGGGATCCCGCGGCGGCTGCTGCTCTGA 1500  
 Qy 1501 GCCGCTGATCCGTA 1515  
 Db 1501 GCCGCTGATCCGTA 1515

RESULT 4

US-10-311-034-33  
 ; Sequence 33, Application US/10311034  
 ; Publication No. US2004002342A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.  
 ; APPLICANT: YUE, Henry  
 ; APPLICANT: LAL, Preeti  
 ; APPLICANT: BANDMAN, Olga  
 ; APPLICANT: BOROWSKY, Mark L.  
 ; APPLICANT: RU-YOUNG, Janice  
 ; APPLICANT: LU, Yan  
 ; APPLICANT: GANDHI, Ameena R.

APPLICANT: TRIBOULEY, Catherine M.  
 APPLICANT: CHAWLA, Narinder K.  
 APPLICANT: YAO, Monique G.  
 APPLICANT: LU, Dyung Aina M.  
 APPLICANT: GREENWALD, Sara R.  
 APPLICANT: RAMKUMAR, Jayalaxmi  
 APPLICANT: GRIFFIN, Jennifer A.  
 APPLICANT: KEARNEY, Liam  
 APPLICANT: BURFORD, Neil  
 APPLICANT: NGUYEN, Dannel B.  
 APPLICANT: TANG, Y. Tom  
 APPLICANT: BAUGHN, Mariah R.  
 APPLICANT: HE, Ann  
 APPLICANT: THORNTON, Michael  
 APPLICANT: HAFALIA, April  
 APPLICANT: ARVIZU, Chandra S.  
 APPLICANT: GURURAJAN, Rajagopal  
 APPLICANT: LO, Terence P.  
 APPLICANT: KHAH, Farrah A.  
 APPLICANT: RECIPON, Shirley A.  
 APPLICANT: AZIMZAI, Yalda  
 APPLICANT: POLICKY, Jennifer L.  
 APPLICANT: DING, Li  
 APPLICANT: GREYER, Megan  
 APPLICANT: ELLIOTT, Vicki S.  
 APPLICANT: THANGAVELU, Kavitha  
 APPLICANT: BATRA, Sajeev  
 APPLICANT: ISON, Craig H.  
 TITLE OF INVENTION: HUMAN KINASES  
 FILE REFERENCE: PI-0125 PCT  
 CURRENT APPLICATION NUMBER: US/10/311,034  
 TITLE OF INVENTION: HUMAN KINASES  
 CURRENT FILING DATE: 2002-12-10  
 PRIOR APPLICATION NUMBER: 60/213,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
 60/228,056  
 PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0-  
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 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: PERL Program  
 SEQ ID NO 33  
 LENGTH: 2056  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: Incyte ID No. US2004002342A1 3951059CB1  
 US-10-311-034-33

Query Match 99.7%; Score 1510.2; DB 16; Length 2066;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1512; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GGGGAGATGTGAAGTTCAAAATATGAGCGCGGAAATCCTTTGGATGCTGTGCTGAA 60  
 Db 8 GGGGAGATGTGAAGTTCAAAATATGAGCGCGGAAATCCTTTGGATGCTGTGCTGAA 67  
 Qy 61 CCCATTGCCAACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACACCTTTATG 120  
 Db 68 CCCATTGCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACACCTTTATG 127  
 Qy 121 ACTCAACAGCAGATGCTCCTCTTTCCGAGAGAGGATATTAGATGCCCTTTTGTTC 180  
 Db 128 ACTCAACAGCAGATGCTCCTCTTTCCGAGAGAGGATATTAGATGCCCTTTTGTTC 187  
 Qy 181 TTTGAAGATGCACTGAGCTGCTGATGAAGATTAAAGCAGCTGAGCACTTTGTCGG 240  
 Db 188 TTTGAAGATGCACTGAGCTGCTGATGAAGATTAAAGCAGCTGAGCACTTTGTCGG 247  
 Qy 241 AAGTATTCGACACCATAGCTGAGTGTACAGGAGCTCCAGCCTTCGGCAAGAGACTTCGAA 300  
 Db 248 AAGTATTCGACACCATAGCTGAGTGTACAGGAGCTCCAGCCTTCGGCAAGAGACTTCGAA 307  
 Qy 301 GTCAGAGTCTTGTAGTGTGCTCACTTTGCTGAGTGCAGTGTGATGAGAGAGCA 360

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 368 ACCGGGACATCTATGCTATGAAAGTGTAGTAAAGAGAGGCTTTATTTGGCCCGAGGACAG 427  
 421 GTTTCATTTTGGAGAGCGGAGCAATATATCTCGAAGCAAGCCCGTGGATCCCC 480  
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 601 CAGTTTACCTAGCTGAGTGTATTTGGCTGTTCACAGCGTTTCACTGATGGGATAGTG 660  
 608 CAGTTTACCTAGCTGAGTGTATTTGGCTGTTCACAGCGTTTCACTGATGGGATAGTG 667  
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 668 CATCGAGATCAAGCCTGAGACATTTCTGTTGACCGCAGCAGACACATCAAGCTGGT 727  
 721 GATTTTGGATCTGCGCGGAAATGAATCAAAACAGATGGTGAATGCCAACTCCCGATT 780  
 728 GATTTTGGATCTGCGCGGAAATGAATCAAAACAGATGGTGAATGCCAACTCCCGATT 787  
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 788 GGGACCCAGATACATGCTCTCTGAGTGTGCTGATGATGATGATGATGATGATGATGATG 847  
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 848 ACCTAGCGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGT 907  
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 968 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGTCTTCTGATGCTGATT 1027  
 1021 CAAAGCTTGTGTGGCCAGAGAGAGAGAGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGT 1080  
 1028 CAAAGCTTGTGTGGCCAGAGAGAGAGAGTGTGAAGTGTGTGTGTGTGTGTGTGTGTGT 1087  
 1081 TTCTTCTTAAATTTGACTGGAAACCAATTCGTAATCTCTCTCTCTCTCTCTCTCTCTCT 1140  
 1088 TTCTTCTTAAATTTGACTGGAAACCAATTCGTAATCTCTCTCTCTCTCTCTCTCTCTCT 1147  
 1141 CTCAGTCCGAGATGACATCTTCAATTTGATGAACCCAGAGAGAGATTCGTGGTTTCA 1200  
 1148 CTCAGTCCGAGATGACATCTTCAATTTGATGAACCCAGAGAGAGATTCGTGGTTTCA 1207  
 1201 TCCTCTCCGTCGAGTGTGAGCCCTCAGGCTTCTCGGTGAAGAACTCCCTTTGTGGGG 1260  
 1208 TCCTCTCCGTCGAGTGTGAGCCCTCAGGCTTCTCGGTGAAGAACTCCCTTTGTGGGG 1267  
 1261 TTTTCTAGCAGAGCCTGGGATTTCTGTGATGATGATGATGATGATGATGATGATGATG 1320  
 1268 TTTTCTAGCAGAGCCTGGGATTTCTGTGATGATGATGATGATGATGATGATGATGATG 1327  
 1321 GACTCCCTCCGAGAGTGTGCTTCAATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 1328 GACTCCCTCCGAGAGTGTGCTTCAATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1387  
 1381 CAGAGCTCTCAGGACAGTGTCAAGAGTATTTATTTCCGAGAGCGGCTCTCTCTCTTGC 1440  
 1388 CAGAGCTCTCAGGACAGTGTCAAGAGTATTTATTTCCGAGAGCGGCTCTCTCTCTTGC 1447

RESULT 5  
 US-10-415-011-43  
 ; Sequence 43, Application US/10415011  
 ; Publication No. US20040053394A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE CORPORATION  
 ; APPLICANT: GURURAJAN, Rajagopal  
 ; APPLICANT: BAUGHN, Mariah R.  
 ; APPLICANT: CHAWLA, Narinder K.  
 ; APPLICANT: ELLIOTT, Vicki S.  
 ; APPLICANT: XU, Yuming  
 ; APPLICANT: ARVIZU, Chandra S.  
 ; APPLICANT: YAO, Monique G.  
 ; APPLICANT: RAMKUMAR, Jayalaxmi  
 ; APPLICANT: DING, Li  
 ; APPLICANT: TANG, Y. Tom  
 ; APPLICANT: HAFALIA, April J.A.  
 ; APPLICANT: NGUYEN, Daniel B.  
 ; APPLICANT: GANDHI, Ameena R.  
 ; APPLICANT: LU, Yan  
 ; APPLICANT: YUE, Henry  
 ; APPLICANT: BURFORD, Neil  
 ; APPLICANT: BANIMAN, Olga  
 ; APPLICANT: TRIBOULEY, Catherine M.  
 ; APPLICANT: LAL, Preeti G.  
 ; APPLICANT: REEPPON, Shirley A.  
 ; APPLICANT: LU, Dyung Aina M.  
 ; APPLICANT: BOROMSKY, Mark L.  
 ; APPLICANT: THURNTON, Michael B.  
 ; APPLICANT: SWANAKER, Anita  
 ; APPLICANT: THANGAVELU, Kavitha  
 ; APPLICANT: KHAN, Farrah A.  
 ; APPLICANT: ISON, Craig H.  
 ; TITLE OF INVENTION: HUMAN KINASES  
 ; FILE REFERENCE: PI-0262 USN  
 ; CURRENT APPLICATION NUMBER: US/10/415,011  
 ; PRIOR FILING DATE: 2003-04-18  
 ; PRIOR APPLICATION NUMBER: PCT/US01/47728  
 ; PRIOR FILING DATE: 2001-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/242,410  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/244,068  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/245,708  
 ; PRIOR FILING DATE: 2000-11-03  
 ; PRIOR APPLICATION NUMBER: US 60/247,672  
 ; PRIOR FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: US 60/249,565  
 ; PRIOR FILING DATE: 2000-11-16  
 ; PRIOR APPLICATION NUMBER: US 60/252,730  
 ; PRIOR FILING DATE: 2000-11-22  
 ; PRIOR APPLICATION NUMBER: US 60/250,807  
 ; PRIOR FILING DATE: 2000-12-01  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 43  
 ; LENGTH: 6298  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CB1  
 ; US-10-415-011-43

Appl  
 Appl

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361 SKIDWNIRNSPPFVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGFSGEELPFVGF 420  
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421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVISAAGLLPCSR 480  
481 ILPSVYAKSGARGCWL 497  
481 ILPSVYAKSGARGCWL 497

RESULT 2  
US-10-238-709-2  
; Sequence 2, Application US/10238709  
; Patent No. 6680188  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-10-238-709-2

Query Match 100.0%; Score 2602; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.4e+242;  
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQSPSLREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQSPSLREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSFVKYSDTIAEQLOEPSAKDFEVRSLVCGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFVKYSDTIAEQLOEPSAKDFEVRSLVCGHFAEVQVVRKATG 120  
Qy 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQOYAFQDKKHLYLVMEYOPGG 180  
Db 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQOYAFQDKKHLYLVMEYOPGG 180  
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Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Qy 241 GSAAKMNSKNVNAKLPITGPDYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAEYMIYGR 300  
Db 241 GSAAKMNSKNVNAKLPITGPDYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAEYMIYGR 300  
Qy 301 SPFAEGTSARTFNIMNFQRLKFPDPPKVSDFDLIQLSCQKRLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNIMNFQRLKFPDPPKVSDFDLIQLSCQKRLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGFSGEELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVISAAGLLPCSR 480  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKVISAAGLLPCSR 480  
481 ILPSVYAKSGARGCWL 497  
481 ILPSVYAKSGARGCWL 497

RESULT 3

US-10-028-946-4  
; Sequence 4, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1958  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-028-946-4

Query Match 93.8%; Score 2440; DB 4; Length 1958;  
Best Local Similarity 99.6%; Pred. No. 5e+226;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQSPSLREGILDALFVLFE 60  
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQSPSLREGILDALFVLFE 60  
Qy 61 ECSQPALMKIKHVSFVKYSDTIAEQLOEPSAKDFEVRSLVCGHFAEVQVVRKATG 120  
Db 61 ECSQPALMKIKHVSFVKYSDTIAEQLOEPSAKDFEVRSLVCGHFAEVQVVRKATG 120  
Qy 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQOYAFQDKKHLYLVMEYOPGG 180  
Db 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQOYAFQDKKHLYLVMEYOPGG 180  
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240  
Qy 241 GSAAKMNSKNVNAKLPITGPDYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAEYMIYGR 300  
Db 241 GSAAKMNSKNVNAKLPITGPDYNAPEVLTVMNGDGKGTGVLCDMWSVGVIAEYMIYGR 300  
Qy 301 SPFAEGTSARTFNIMNFQRLKFPDPPKVSDFDLIQLSCQKRLKFEGLCCHPFF 360  
Db 301 SPFAEGTSARTFNIMNFQRLKFPDPPKVSDFDLIQLSCQKRLKFEGLCCHPFF 360  
Qy 361 SKIDWNIRNSPPFVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGFSGEELPFVGF 420  
Db 361 SKIDWNIRNSPPFVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGFSGEELPFVGF 420  
Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468  
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKV 468

RESULT 4  
US-10-028-946-2  
; Sequence 2, Application US/10028946  
; Patent No. 6734009  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/028,946  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; NUMBER OF SEQ ID NOS: 4

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**This Page Blank (uspto)**



**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 04:23:00 ; Search time 154 Seconds  
(without alignments)  
6992.501 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1 9999agatgttgagttcaaa.....tttgagcgcgtgatccgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1515	100.0	1515	4	US-09-804-471A-1
2	1515	100.0	1515	4	US-10-238-709-1
3	1398.2	92.3	5877	4	US-10-028-946-3
4	1398.2	92.3	6165	4	US-10-028-946-1
5	963.2	63.6	2162	4	US-09-774-528-419
6	760.8	50.2	1133	4	US-09-916-204-1
7	760.8	50.2	1133	4	US-10-282-048-1
8	225.6	14.9	2726	2	US-08-422-699A-12
9	225.6	14.9	2726	2	US-08-422-706B-12
10	218.8	14.4	2511	2	US-08-422-699A-8
11	218.8	14.4	2511	2	US-08-422-706B-8
12	218.4	14.4	3182	1	US-08-484-044-11
13	216.2	14.3	174493	4	US-09-804-471A-3
14	216.2	14.3	174493	4	US-10-238-709-3
15	194	12.8	2706	2	US-08-630-822A-61
16	194	12.8	2706	2	US-09-005-069-61
17	194	12.8	2706	3	US-09-171-156A-20
18	194	12.8	2706	4	US-09-004-730A-20
19	194	12.8	2706	4	US-08-981-799A-20
20	186	12.3	4363	2	US-08-685-576-5
21	184.4	12.2	4848	4	US-09-976-594-295
22	178.8	11.8	48763	4	US-09-916-204-3
23	178.8	11.8	48763	4	US-10-282-048-3
24	175.4	11.6	4065	4	US-09-016-434-1105
25	175.4	11.6	4739	3	US-08-685-871-1
26	171.6	11.3	5053	2	US-08-685-576-2
27	156.4	10.3	3323	2	US-08-422-699A-10

28	156.4	10.3	3323	2	US-08-422-706B-10
29	125.8	8.3	3155	3	US-09-442-100-7
30	125.8	8.3	3155	4	US-08-939-106-7
31	125.8	8.3	3155	4	US-09-442-102-7
32	125.4	8.3	1498	3	US-09-509-902A-6
33	125.4	8.3	1961	3	US-09-509-902A-15
34	125.4	8.3	5276	4	US-09-233-857-2
35	121	8.0	3018	2	US-08-860-150-6
36	121	8.0	3018	3	US-09-338-132-6
37	114.6	7.6	1935	3	US-08-878-989-11
38	114.6	7.6	1935	3	US-09-272-736-11
39	113	7.5	3213	3	US-09-442-100-5
40	113	7.5	3213	4	US-08-939-106-5
41	113	7.5	3213	4	US-09-442-102-5
42	110.4	7.3	1251	4	US-09-248-796A-4400
43	108	7.1	2160	3	US-09-588-256-1
44	104.6	6.9	5720	3	US-09-442-100-1
45	104.6	6.9	5720	4	US-08-939-106-1

ALIGNMENTS

RESULT 1  
US-09-804-471A-1  
; Sequence 1, Application US/09804471A  
; Patent No. 6479269  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01164  
; CURRENT APPLICATION NUMBER: US/09/804.471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-09-804-471A-1

Query Match	100.0%	Score 1515;	DB 4;	Length 1515;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 1515;	Conservative 0;			Gaps 0;
Qy	1	GGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA	60	
Db	1	GGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA	60	
Qy	61	CCCATTCGCAACCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATG	120	
Db	61	CCCATTCGCAACCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATG	120	
Qy	121	ACTCAACAGCAGATGCTCTCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC	180	
Db	121	ACTCAACAGCAGATGCTCTCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTC	180	
Qy	181	TTTGAAGATGCACTGAGCTGCTCTGATGAAGATTAAAGCAGTGAACATTTGTCGG	240	
Db	181	TTTGAAGATGCACTGAGCTGCTCTGATGAAGATTAAAGCAGTGAACATTTGTCGG	240	
Qy	241	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGAGCTTCGAA	300	
Db	241	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGAGCTTCGAA	300	
Qy	301	GTCAGAGTCTTGTAGGTTGTGTCCTTTGCTGAAGTGAAGTGAAGAGAAAGCA	360	
Db	301	GTCAGAGTCTTGTAGGTTGTGTCCTTTGCTGAAGTGAAGTGAAGAGAAAGCA	360	
Qy	361	ACCGGGACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGGCCAGGACAG	420	

Db 361 ACCGGGACATCTATGCTATGAAAGTGAAGAAAGGGCTTTATTGGCCCGAGGACG 420  
QY 421 GTTTCATTTTTCAGGAGAGCGGACATATATCTCGACGACAAAGCCCGTGGATCCC 480  
Db 421 GTTTCATTTTTCAGGAGAGCGGACATATATCTCGAAGACAAAGCCCGTGGATCCC 480  
QY 481 CAATTACAGTATGCTTTTCAGGACAAAATCAACCTTTATCTGGTCAATGAAATACAGCCT 540  
Db 481 CAATTACAGTATGCTTTTCAGGACAAAATCAACCTTTATCTGGTCAATGAAATACAGCCT 540  
QY 541 GGAGGGAGCTTCTGTCTACCTTTTGAATAGATAGAGGACCAAGTATAGTAAACCTGATA 600  
Db 541 GGAGGGAGCTTCTGTCTACCTTTTGAATAGATAGAGGACCAAGTATAGTAAACCTGATA 600  
QY 601 CAGTTTACTAGCTAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTG 660  
Db 601 CAGTTTACTAGCTAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTG 660  
QY 661 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGGACAGGACACATCAAGCTGGT 720  
Db 661 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGGACAGGACACATCAAGCTGGT 720  
QY 721 GATTTTGGATCTGCCCGGAAATGAATTCARAAAGATGGTGAATGCCAAACTCCCGATT 780  
Db 721 GATTTTGGATCTGCCCGGAAATGAATTCARAAAGATGGTGAATGCCAAACTCCCGATT 780  
QY 781 GGGACCCAGATTACATGGCTCTCTGAAGTCTGATGTAAGACGGGGATGGAAGGC 840  
Db 781 GGGACCCAGATTACATGGCTCTCTGAAGTCTGATGTAAGACGGGGATGGAAGGC 840  
QY 841 ACCTAGCGCTGACGTGACCTGGTGTGACGTGGCGGTGATGGCTATGAGATGATTTAT 900  
Db 841 ACCTAGCGCTGACGTGACCTGGTGTGACGTGGCGGTGATGGCTATGAGATGATTTAT 900  
QY 901 GGGAGATCCCCCTTCGACAGGGAACCTCTGCCAGAACCTTCATTAACATTTATGAATTC 960  
Db 901 GGGAGATCCCCCTTCGACAGGGAACCTCTGCCAGAACCTTCATTAACATTTATGAATTC 960  
QY 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTCTTCTGATCTGAT 1020  
Db 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAAGTCTTCTGATCTGAT 1020  
QY 1021 CAAAGCTTGTGTGGCGGACAGAAAGAGACACTGAAGTCTTGAAGTCTTGTGCTGCATCCT 1080  
Db 1021 CAAAGCTTGTGTGGCGGACAGAAAGAGACACTGAAGTCTTGAAGTCTTGTGCTGCATCCT 1080  
QY 1081 TTCTTCTCTAAATTTGACTGGAAACAACTTCGTAATCTCTCTCCCGCTTCTTCCAC 1140  
Db 1081 TTCTTCTCTAAATTTGACTGGAAACAACTTCGTAATCTCTCTCTCCCGCTTCTTCCAC 1140  
QY 1141 CTCAGTCCGACGATGACACCTTCAATTTTGAATGACCAAGAGAAATTCGTGGGTTTCA 1200  
Db 1141 CTCAGTCCGACGATGACACCTTCAATTTTGAATGACCAAGAGAAATTCGTGGGTTTCA 1200  
QY 1201 TCCTCTCCGTCCGACGTGACCCCTCAGCTTCTCGGTTGAAGAACTGCGCTTGTGGG 1260  
Db 1201 TCCTCTCCGTCCGACGTGACCCCTCAGCTTCTCGGTTGAAGAACTGCGCTTGTGGG 1260  
QY 1261 TTTTCGTACAGCAGCAGTGGGATCTTGTGAGATCTGAGTCTGTTGTGTCGGGCTG 1320  
Db 1261 TTTTCGTACAGCAGCAGTGGGATCTTGTGAGATCTGAGTCTGTTGTGTCGGGCTG 1320  
QY 1321 GACTCCCTCTGCCAAGACTAGCTCCATGTAAGAAATCTTCTCATCAAAAGCAAGAGCTA 1380  
Db 1321 GACTCCCTCTGCCAAGACTAGCTCCATGTAAGAAATCTTCTCATCAAAAGCAAGAGCTA 1380  
QY 1381 CAAAGCTCTCAGACAAAGTGTCAAGGATTTATTTCCGACGCGGCTCTCTCTTGC 1440  
Db 1381 CAAAGCTCTCAGACAAAGTGTCAAGGATTTATTTCCGACGCGGCTCTCTCTTGC 1440  
QY 1441 TCCAGGATCTCCCGTCCGTATATGCAAGGATCCGCGCGGCGGCTGCTGGCTCTGA 1500  
Db 1441 TCCAGGATCTCCCGTCCGTATATGCAAGGATCCGCGCGGCGGCTGCTGGCTCTGA 1500

QY 1501 GCCGCCTGATCCGTA 1515  
Db 1501 GCCGCCTGATCCGTA 1515

## RESULT 2

US-10-238-709-1  
; Sequence 1, Application US/10238709  
; Patent No. 6680188  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164DIV  
; CURRENT APPLICATION NUMBER: US/10/238,709  
; CURRENT FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
US-10-238-709-1

Query Match 100.0%; Score 1515; DB 4; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTTGGATGCTGCTGCTGAA 60  
Db 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTTGGATGCTGCTGCTGAA 60  
QY 61 CCATTGCCAACCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTATG 120  
Db 61 CCATTGCCAACCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTATG 120  
QY 121 ACTCAACAGCAGATGTCCTCTTCCGAGAGAGGATATTAGATCCCTCTTTGTTCTC 180  
Db 121 ACTCAACAGCAGATGTCCTCTTCCGAGAGAGGATATTAGATCCCTCTTTGTTCTC 180  
QY 181 TTTGAAGATGCACTGAGTCTGCTCTGATGAAGATTAAGCACTGAGCAACTTGTCCGG 240  
Db 181 TTTGAAGATGCACTGAGTCTGCTCTGATGAAGATTAAGCACTGAGCAACTTGTCCGG 240  
QY 241 AAGTATTCGACACCATAGCTGAGTTACAGGACTCCAGCTTCGCAAGAGACTTCGAA 300  
Db 241 AAGTATTCGACACCATAGCTGAGTTACAGGACTCCAGCTTCGCAAGAGACTTCGAA 300  
QY 301 GTCAGAACTCTTGTAGTGTGCTGCTTGTCTGAAGTGCAGGTGTTAAGAGAAAGCA 360  
Db 301 GTCAGAACTCTTGTAGTGTGCTGCTTGTCTGAAGTGCAGGTGTTAAGAGAAAGCA 360  
QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGCTTTATTTGGCCCGAGGACG 420  
Db 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGCTTTATTTGGCCCGAGGACG 420  
QY 421 GTTTCATTTTTTCAGGAAGAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGGATCCC 480  
Db 421 GTTTCATTTTTTCAGGAAGAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGGATCCC 480  
QY 481 CAATTACAGTATGCTTTTCAGGACAAAATCAACCTTTATCTGGTCAATGAAATACAGCCT 540  
Db 481 CAATTACAGTATGCTTTTCAGGACAAAATCAACCTTTATCTGGTCAATGAAATACAGCCT 540  
QY 541 GGAGGGAGCTTCTGTCTACCTTTTGAATAGATAGAGGACCAAGTATAGTAAACCTGATA 600  
Db 541 GGAGGGAGCTTCTGTCTACCTTTTGAATAGATAGAGGACCAAGTATAGTAAACCTGATA 600  
QY 601 CAGTTTACTAGCTAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTG 660  
Db 601 CAGTTTACTAGCTAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGGATACGTG 660







Matches 762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 60  
 Db 48 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 107  
 QY 61 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCCCTTTATG 120  
 Db 108 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCCCTTTATG 167  
 QY 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 180  
 Db 168 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 227  
 QY 181 TTGGAAGATGAGTCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 240  
 Db 228 TTGGAAGATGAGTCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 287  
 QY 241 AAGTATTCGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 300  
 Db 288 AAGTATTCGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 347  
 QY 301 GTCAGAGTCTTGTAGTTGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 360  
 Db 348 GTCAGAGTCTTGTAGTTGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 407  
 QY 361 ACCGGGACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGCAG 420  
 Db 408 ACCGGGACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGCAG 467  
 QY 421 GTTTCATTTTTCGAGGAGCGGAAACATATTATCTCGAAGCACAAGCCGCTGGATCCCC 480  
 Db 468 GTTTCATTTTTCGAGGAGCGGAAACATATTATCTCGAAGCACAAGCCGCTGGATCCCC 527  
 QY 481 CAATTACAGTATGCTCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 540  
 Db 528 CAATTACAGTATGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 587  
 QY 541 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTATGATGAAACCTGATA 600  
 Db 588 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTATGATGAAACCTGATA 647  
 QY 601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCTTCACTCTGATGGATACGTTG 660  
 Db 648 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCTTCACTCTGATGGATACGTTG 707  
 QY 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720  
 Db 708 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 767  
 QY 721 GATTTTGGATCTCCCGGAAATGAATTCAAACAAGATGGTAA 764  
 Db 768 GATTTTGGATCTCCCGGAAATGAATTCAAACAAGATGGTAA 811

RESULT 7  
 US-10-282-048-1  
 ; Sequence 1, Application US/10282048  
 ; Patent No. 662948  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wei, Ming-Hui et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; THEREOF  
 ; FILE REFERENCE: CL001164CIP-DIV  
 ; CURRENT APPLICATION NUMBER: US/10/282, 048  
 ; CURRENT FILING DATE: 2002-10-29  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1133  
 ; TYPE: DNA  
 ; ORGANISM: Human

US-10-282-048-1

Query Match 50.2%; Score 760.8; DB 4; Length 1133;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-244;  
 Matches 762; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 60  
 Db 48 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGGTCTGCTGAA 107  
 QY 61 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTTTCCAGGGGAAACCAACCCCTTTATG 120  
 Db 108 CCATTGCGCAACCGGCGCTCCAGGCTGAATCTGTTCTTTCCAGGGGAAACCAACCCCTTTATG 167  
 QY 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 180  
 Db 168 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 227  
 QY 181 TTGGAAGATGAGTCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 240  
 Db 228 TTGGAAGATGAGTCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 287  
 QY 241 AAGTATTCGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 300  
 Db 288 AAGTATTCGACACCATAGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 347  
 QY 301 GTCAGAGTCTTGTAGTTGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 360  
 Db 348 GTCAGAGTCTTGTAGTTGCTGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 407  
 QY 361 ACCGGGACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGCAG 420  
 Db 408 ACCGGGACATCTATGCTATGAAAGTGAAGAGAGGCTTTATTTGGCCCGAGGAGCAG 467  
 QY 421 GTTTCATTTTTCGAGGAGCGGAAACATATTATCTCGAAGCACAAGCCGCTGGATCCCC 480  
 Db 468 GTTTCATTTTTCGAGGAGCGGAAACATATTATCTCGAAGCACAAGCCGCTGGATCCCC 527  
 QY 481 CAATTACAGTATGCTCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 540  
 Db 528 CAATTACAGTATGCTCTCTTTCCGAGAGGGATATTAGATCCCTCTTTGTTCTC 587  
 QY 541 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTATGATGAAACCTGATA 600  
 Db 588 GGAGGGAGCTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTATGATGAAACCTGATA 647  
 QY 601 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCTTCACTCTGATGGATACGTTG 660  
 Db 648 CAGTTTACCTAGCTGAGCTGATTTTGGCTGTTTCAAGCTTCACTCTGATGGATACGTTG 707  
 QY 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720  
 Db 708 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 767  
 QY 721 GATTTTGGATCTCCCGGAAATGAATTCAAACAAGATGGTAA 764  
 Db 768 GATTTTGGATCTCCCGGAAATGAATTCAAACAAGATGGTAA 811

RESULT 8  
 US-08-422-699A-12  
 ; Sequence 12, Application US/08422699A  
 ; Patent No. 5955265  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brook, J. David  
 ; APPLICANT: Housman, David E.  
 ; APPLICANT: Shaw, Duncan J.  
 ; APPLICANT: Harley, Keith J.  
 ; APPLICANT: Johnson, Keith J.  
 ; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC  
 ; DYSTROPHY GENE AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:

ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

ZIP: 02713

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/422,699A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/422,706

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/023,612

FILING DATE: 26-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/839,255

FILING DATE: 20-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/01545

FILING DATE: 19-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00253

FILING DATE: 05-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB9202485.0

FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5830A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2726 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-422-699A-12

Query Match 14.9%; Score 225.6; DB 2; Length 2726;

Best Local Similarity 54.0%; Pred. No. 1.3e-64;

Matches 534; Conservative 0; Mismatches 439; Indels 15; Gaps 3;

QY 200 CTGCTCTGATGAAGATTAGCAGTGGAGCACTTTGTCGGAAGTATTCGGACACATAG 259  
DB 243 CCGAATGGCCCGAGGACAGTACGTGGCGACTTCTTGAGTGGGGGAGCCCATCGTG 302  
QY 260 CTGAGTTACAGGAGCTCCAGCCCTTCGCAAGACATTCGAAGTCACAGTCTTGAGTT 319  
DB 303 TGAGGCTTAAGAGGTCCTGCTACAGGAGGACATTCAGATCTGAAGGTGATCGGAC 362  
QY 320 GTGGTCACTTTGCTGAAGTGCAGTGGTGAAGAGAGAAACACCGGGGACATCTATGCTA 379  
DB 363 GCGGGGCGTTTCCAGGAGTACGCGGTAGTGAAGATGAAGACAGCGGCGGAGTATGCCA 422  
QY 380 TGAAGTGAAGAGAGAGGCTTTATTCGCCCGGAGGAGGTTTCATTTTGGAGAG 439  
DB 423 TGAAGATCAAGACAGTGGAGCATGCTGAAGAGGGGCGAGGTGCTGCTCCGTTGAGG 482  
QY 440 AGCGGAACATATTTATCTCGAAGACACAGCCCGGTGGATCCCCCAATTACAGTATGCTTTC 499  
DB 483 AGAGGACGCTGTTGGTGAATGGGACCGCGGTGGATCAGCAGCTGCATCTCGCTTCC 542  
QY 500 AGGACAAAAATACCTTTTATCTGTCATGAATATCAGCTGGAGGGGACTTGCTGTAC 559

DB 543 AGGATGAGAACTACCTGTACCTGTACCTGTACCTGTACCTGTACCTGTACCTGTAC 602  
QY 560 TTTTGAATAGATATGAGGACCACTTAGTAAACCTGATACAGTTTACCTAGCTGAGC 619  
DB 603 TGCTGAGCAAGTTTGGGAGCGGATTCCGCCGAGATGGCGCTTCTACCTGCGGAGA 662  
QY 620 TGATTTTGGCTGTTTACAGCGCTTCTATCTGATGGGATACCTGATCGAGACATCAAGCTG 679  
DB 663 TTGTCATGGCCATAGACTCGGTGCACCGCTTGGCTAGCTGCACAGGACATCAACCG 722  
QY 680 AGAACATTTCTGTTGACCGGACAGACACATCAAGCTGCTGGATTTGGATCTCCCGGA 739  
DB 723 ACAACATCTCTGTCGACCGCTGTGGCCACATCCCGCTGGCGACTTGGCTCTTGCCTCA 782  
QY 740 AAATGAATTTCAACAAGATGGTGAATGCCAACTCCCGATTGGGACCCAGATACATGG 799  
DB 783 AGCTGGGCGAGATGGAACTGGTGGCTGGTGGCTGGGACCCAGACTACCTGT 842  
QY 800 CTCCTGAAGTCTGA---CTGTGATGAACGGGGATGAAAGGACCTACCGCTTGGACT 856  
DB 843 CCCCCGAGATCTGCAGGCTGTGGCGGTGGGCTGGGACAGGAGCTACCGGCGCGAGT 902  
QY 857 GTGACTGGTGTCTAGTGGGCGTGTGCTATGATGATGATTTATGGGAGATCCCGCTTCG 916  
DB 903 GTGACTGGTGGGCGTGGTGTATTCGCTATGAATGTTCTATGGGAGACGCGCTTCT 962  
QY 917 CAGAGGGAACCTCTGCCAGAACCTTCAATACATTATGAATTTCCAGCGGTTTTTGAAT 976  
DB 963 ACGCGGATTCACGCGGAGACCTATGCAAGATCGTCCACATCAAGAGCACCTCTCTC 1022  
QY 977 TTCCAGATGACCCCAAGTGAAGT---GACTTCTGTGATCTGATTCATCAAGCTTGTGT 1033  
DB 1023 TGCCGCTGGTGGAGGAGGCTCCCTGAGGAGGCTCGAGACTTCATTCAGCGGTGCTGT 1082  
QY 1034 GCGGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGC-----CATCCTTTCT 1084  
DB 1083 GTCCCCCGAGACACGCTGGCGCGGTGGAGAGGAGCTTCGGAGACATCCCTTCT 1142  
QY 1085 TCTCTAAATTTGACTGGAACAACTTCGTAACTCTCTCCCGCTTGGTTCCTCCACCTCA 1144  
DB 1143 TCTTTGGCTCGACTGGGATGCTCTCGGGACAGCGTGGCGGCTTTTACACCGGATTCG 1202  
QY 1145 AGTCGCGATGACACCTCCAAATTTGA 1172  
DB 1203 AAGTGCCACCGACATGCAACTCGA 1230

#### RESULT 9

US-08-422-706B-12

Sequence 12, Application US/08422706B

Patent No. 5977333

GENERAL INFORMATION:

APPLICANT: Brook, J. David

APPLICANT: Housman, David E.

APPLICANT: Shaw, Duncan J.

APPLICANT: Harley, Helen G.

APPLICANT: Johnson, Keith J.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

ZIP: 02713

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30





	APPLICATION NUMBER:	US 07/839,255	
	FILING DATE:	20-FEB-1992	
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER:	PCT/US93/01545	
	FILING DATE:	19-FEB-1993	
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER:	PCT/GB93/00253	
	FILING DATE:	05-FEB-1993	
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER:	GB9202485-0	
	FILING DATE:	06-FEB-1992	
	ATTORNEY/AGENT INFORMATION:		
	NAME:	Granahan, Patricia	
	REGISTRATION NUMBER:	32,227	
	REFERENCE/DOCKET NUMBER:	MIT-5830A2	
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE:	617-861-6240	
	TELEFAX:	617-861-9540	
	INFORMATION FOR SEQ ID NO:	8:	
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	2511 base pairs	
	TYPE:	nucleic acid	
	STRANDEDNESS:	double	
	TOPOLOGY:	linear	
	MOLECULE TYPE:	DNA (genomic)	
	FEATURE:		
	NAME/KEY:	CDS	
	LOCATION:	1..1746	
	US-08-422-699A-8		
	Query Match	14.4%; Score 218.8; DB 2; Length 2511;	
	Best Local Similarity	54.5%; Pred.No. 2.4e-62;	
	Matches 511; Conservative	0; Mismatches 412; Indels 15; Gaps 3	
QY	250	GACACCATAGCTGAGTTACAGAGGCTTCAGGCCTTCGCCAAAGCACTTCGGAGTCCAGAGT	309
DB	43	GCACATCGTGTCGAGGCTTAAGAGGTCCGACTGCAGAGGACGACATTCGAGATTCTGAAG	102
QY	310	CTTTAGAGTTGTGGTCACTTTTGCTCAAGTCAGGTGCTTAAGAGAGAAAGCAACCGGGGAC	369
DB	103	GTGATCGGACGCGGGCGCTTCAGCGAGTAGTCGGTAGTGAAGATGAAGACAGCGGCCAG	162
QY	370	ATCTATGCTATAAGAGTGAAGAAGAGCCTTTATGGCCACGAGGACAGGTTTCATTT	429
DB	163	GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGCGAGGTGTCTGC	222
QY	430	TTTGAGGAAGACGGAAACATATTCTCGAAGCACAAAGCCGCTGGATCCCCCAATTACAG	489
DB	223	TTCGCTGAGAGAGGAGCGTGTGTGTAATGGGACCCGGCGGTGGATCACCAGCTGCAC	282
QY	490	TATGCTTTACGACAAAATCACTTTATCTGTCATGGAATATCAGCCTTGGAGGGGAC	549
DB	283	TTCCGCTCCAGGATGAGAACTACTCTGTACCTGCTCATGGATATTACGTGGCGGGGAC	342
QY	550	TTGCTGTCACTTTTCAATAGATATGAGACCAAGTTAGATGAAACCTGATACAGTTTTAC	609
DB	343	CTGCTGACACTGCTGAGCAAGTTTGGGAGCGGAATCCGGCCGAGATGGCGCGCTTCTAC	402
QY	610	CTAGCTGAGCTGATTTGGCTGTTCCACAGCGTTTCATCTGATGGGATACGTGCATCGAGAC	669
DB	403	CTGGCGGAGATTGTATGCCCATAGACTCGGTCGACCGGTTTGGCTACGTGCACAGGAC	462
QY	670	ATCAAGCTGAGAACTTCTGTTTACCGCACAGGACACATCAAGCTGGTGGATTTTGA	729
DB	463	ATCAAAACCGGACAACTCCTGCTGACCGCTGTGGCCACATCCGCTTGGCCGACTTCGGC	522
QY	730	TTCTCCCGCAAAATCAATTCAAAAGATGCTGTAATGCCAACTCCCGATTGGGACCCCA	789
DB	523	TCTTGGCTCAAGCTCGGGCAGATGGAACGTCGCTGGTGGCTGTGGGACACCCCA	582
QY	790	GATTACATGGCTCTTGA---AGTGTGATCTGTGATGAACGGGGATGAAAGGCACTTAC	846
DB	583	GACTACTCTGCCCGGATCCTGAGGCTCTGGGCGGTGGGCTCGGACAGCAGCTAC	642

ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-5830A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2511 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1746  
US-08-422-706B-8

Query Match 14.4%; Score 218.8; DB 2; Length 2511;  
Best Local Similarity 54.5%; Pred. No. 2.4e-62;  
Matches 511; Conservative 0; Mismatches 412; Indels 15; Gaps 3;

QY 250 GACACCATAGCTGAGTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAGT 309  
DB 43 GCATCGTGTGAGGCTTAAGGAGGTCCAGCTGCAGAGGAGACTTCGAGATTCTGAAG 102  
QY 310 CTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAACCAACCGGGAC 369  
DB 103 GTGATCGGACGGGGCGTTTCAGCAGGTAGCGGTAGTGAAGATGAAGCAGACGGCCAG 162  
QY 370 ATCTATGCTATGAAGTATGAAGAAGAGGCTTTATGGCCAGGAGCAGGTTTCATTT 429  
DB 163 GTGATATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGGGAGGTGCTGC 222  
QY 430 TTTGAGGAGAGCGGAACTATTATCTCGAAGCACAAGCCGCTGGATCCCCCAATACAG 489  
DB 223 TTCCGTGAGGAGGAGCGCTGTTGTTGATGGGACCGCGGTGATCAGCAGCTGCAC 282  
QY 490 TATGCCCTTCAGAGCAAAATACCTTTATCTGGTATGGAATATCAGCCTGGAGGGGAC 549  
DB 283 TTGCGCTTCAGGATGAGAACTACCTGTACTCTGCTGCTGATGAGTATTACGTGGCGGGAC 342  
QY 550 TTCTGCTCACTTTTGAATAGATATGAGGACCAAGTTAGATGAACCTGATACAGTTTAC 609  
DB 343 CTGCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGGCCGCGATGGCGGCTTCTAC 402  
QY 610 CTAGCTGAGCTGATTTTGGCTGTTCAAGCGTTTCATGATGGGATAGCTGATCGATCGAG 669  
DB 403 CTGGCGGAGATTGTCATGGCCATAGACTCGGTGACCGGCTTTGGTACGTGACACAGGAC 462  
QY 670 ATCAGCCTGAGAACATTCGTTGATGACCGCAGAGACATCAAGCTGGTGGATTGGA 729  
DB 463 ATCAACCCGCAACATCTCTGACCGCTGTGGCCATCCGCTGGCGGACTTCGCG 522  
QY 730 TCTGCCCGGAAATGAATTCACAAAGATGGTGAATGCAAACTCCCGATTGGGACCCCA 789  
DB 523 TCTTGCTCAAGTGGCGGCGAGATGAAGCGGTGCGTGGTGGCTGTGGCACCCCA 582  
QY 790 GATTACATGGCTCTGA---AGTGTGACTGTGATGAACGGGATGGAAGGACCTAC 846  
DB 583 GACTACCTGTCCCGGAGATCTCGAGGCTGTGGCGGTGGGCGCTGGGACAGGAGCTAC 642  
QY 847 GGCCTGAGCTGACTGGTGGTGCAGTGGGCGGATGCTGATGATGATATTATGGGAGA 906  
DB 643 GGGCCCGAGTGTGACTGGTGGGCGGTGGGTGATTCGCTATGAATGTTCTATGGGAG 702  
QY 907 TCCCTTCGAGAGGGAACTCTGCGCAGAACCTTCAATATACATTAATTAATTCAGGGG 966  
DB 703 ACGCCCTTACCGGAGATTCCACGGCGGAGACCTATGGCAAGATCGTCCACTACAAGGAG 762  
QY 967 TTTTGAATTTCCAGATGACCCCAAGATGAGCAGT---GACTTCTTGATCTGATCAA 1023

DB 763 CACCTCTCTGCGCTGGTGGAGGAAGGGTCCCTGAGGAGGCTCGAGACTTCATTAC 822  
QY 1024 AGCTTGTGTGGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC----- 1074  
DB 823 CGGTTGCTGTGTCCCGGAGACACCGCTGGCGGGGTGGAGCGGAGCTTCCGAGACA 882  
QY 1075 CATCCTTTCTCTCTAAATTTGACTGGAAACAACATTCGTAACTCTCTCCCTCCCTTCGTT 1134  
DB 883 CATCCTTTCTCTTTGGCTCGACTGGATGGTCTCGGAGCAGCGGTGCGCTTTACA 942  
QY 1135 CCCACCTCAAGTCCGACGATGACACCTCCAAATTTGA 1172  
DB 943 CCGGATTTGGAAGGTGCCCGGACACATGCAACTTCGA 980

RESULT 12  
US-08-484-044-11  
Sequence 11, Application US/08484044  
Patent No. 5552282  
GENERAL INFORMATION:  
APPLICANT: Caskey, C. T.  
APPLICANT: Fu, Ying-Hui  
APPLICANT: Friedman, David L.  
APPLICANT: Pizzuti, Antonio  
APPLICANT: Fenwick, Raymond G.  
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski, L.L.P.  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,044  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/019,940  
FILING DATE: 19-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5443  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3182 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-044-11

Query Match 14.4%; Score 218.4; DB 1; Length 3182;  
Best Local Similarity 54.5%; Pred. No. 3.8e-62;  
Matches 510; Conservative 0; Mismatches 411; Indels 15; Gaps 3;

QY 252 CACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAAGTCAGAGTCT 311  
DB 743 CATCGTGGTGAAGGCTTAAGGAGGTCCGACTGCGAGAGGAGCGACTTCGAGATTCTGAAGGT 802  
QY 312 TGATGTTGGTCACTTTGCTGAGTGCAGGTGGTAAAGAGAAAGCAACCGGGACAT 371

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Db      803  GATCGGACGGGGCGTTACGAGGTAGCGGTAGTGAAGATGAACAGACGGCGCAGGT 862
Qy      372  CTATGCTATGAAGATGATGAAGAGAGGCTTTATTGGCCCGAGGACAGGTTTCATTTT 431
Db      863  GTATGCATGAAGTATGATGAAGTGGGACATGCTGAAGAGGGGAGGTGCTGCTT 922
Qy      432  TGAGGAAGCGGAACATATATCTCGAAGCAAGCCCGTGTGATCCCAATACAGTA 491
Db      923  CCGTGAGGAGGAGGACGTGTGTGTGAATGGGACCGCGGTGGATCACGACGTGCAC 982
Qy      492  TGCCCTTCAGACAAATAATCACTTTATCTGGTCAATGAATATACGCTGGAGGGAC 551
Db      983  CGCCTTCAGAGATGAGACTACCTGTACCTGTGTCATGGAGTATACGTGGCGGAC 1042
Qy      552  GCTGTACTTTTGAATAGATATGAGGACCAAGTATGAAACCTGATACAGTTTAC 611
Db      1043  GCTGACACTGCTGAGCAAGTTTGGGAGCGGATTCGGCGCGAGATGGCGGCTT 1102
Qy      612  AGTGAGCTGATTTTGGCTGTTACAGCGTTCTATGATGGGATAGTGCATCGACAT 671
Db      1103  GCGGAGATTTGATGGCCATAGACTCGGTGACCGGCTTGGCTAGTGCACAGGACAT 1162
Qy      672  CAAGCTTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTT 731
Db      1163  CAACCCGACAAACATCTGTGACCGCTGTGCGCACATCCGCTGGCGACTTGGCT 1222
Qy      732  TGGCGGAAATGAAATCAACAGATGTTGAATGCCAACTCCGATTTGGGACCCAGA 791
Db      1223  TTGCTCAAGCTCGGGCGAGATGAACGGTGGCGTGGTGGCTGTGGCGACCCCGA 1282
Qy      792  TTACATGGCTCCTGA---AGTGTGACTGTGATGAACGGGGATGGAAGGACAC 848
Db      1283  CTACCTGTCCCGAGATCTCGAGGCTGTGGCGGTGGCTGGGACAGGACGTACGG 1342
Qy      849  CTTGGACTGTGCTGGTGTGCTGAGTGGCGGTGATGCTATGATGATGATTTAT 908
Db      1343  GCGGAGTGTGCTGGTGGCGGTGCTGCTGCTATGAAATGTTCTATGGGACAG 1402
Qy      909  CCCTTCGAGAGGACCTCTCCAGACCTTCAATAACATTAATTTTCAGCGGTT 968
Db      1403  GCCCTTACCGGATTCACGGCGGAGACTATGGAGATGCTCCACATCAAGAGCA 1462
Qy      969  TTTGAAATTTCCAGATACCCCAAGATGAGCAGT---GACTTTCTGATCTGAT 1025
Db      1463  CCTCTCTCTGCGTGTGGACGAGGGTCCCTGAGAGGCTCGAGACTTCAATCAG 1522
Qy      1026  CTTGTTTGGCGGACAGAGAGACTGAAGTTTGAAGTCTTGTGCTG-----CA 1076
Db      1523  GTTGTCTGTCTCCCGGAGACACGGCTGGGCGGGGTGGAGCGGAGCTTCCGGACA 1582
Qy      1077  TCCTTTCTTCTCTAAATTTGACTGGAAACAACTTCGTAATCTCCTCCCTCCCT 1136
Db      1583  TCCCTTCTTCTTGGCCTCGACTGGGATGGTCTCCGGGACAGCGTGCCTTTACAC 1642
Qy      1137  CACCTCAAGTCGACGATGACACTCCAAATTTGA 1172
Db      1643  GGATTCGAAGGTGCCACCGACATGCAACTTCGA 1678

RESULT 13
US-10-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0

```

```

; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match      14.3%; Score 216.2; DB 4; Length 174493;
Best Local Similarity 96.5%; Pred. No. 3.5e-60;
Matches 221; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1287  TCTTGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGCTCCAT 1346
Db      171282  TTTTCTCTACCTAGGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGCTCCAT 171341
Qy      1347  GGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCA 1406
Db      171342  GGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCA 171401
Qy      1407  GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCCGTCCGTATATGC 1466
Db      171402  GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCCGTCCGTATATGC 171461
Qy      1467  CAAGGGATCCGCGCGCGCTGCTGCTCTGAGCCGCTGATCCGTA 1515
Db      171462  CAAGGGATCCGCGCGCGCTGCTGCTCTGAGCCGCTGATCCGTA 171510

RESULT 14
US-10-238-709-3
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

Query Match      14.3%; Score 216.2; DB 4; Length 174493;
Best Local Similarity 96.5%; Pred. No. 3.5e-60;
Matches 221; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1287  TCTTGTAGATCTGAGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGCTCCAT 1346
Db      171282  TTTTCTCTACCTAGGTCTGTGTGTCGGGTCTGGACTCCCTGCCAAGACTAGCTCCAT 171341
Qy      1347  GGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCA 1406
Db      171342  GGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCA 171401
Qy      1407  GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCCGTCCGTATATGC 1466
Db      171402  GGTATTTATTTCCGAGCGCGCTCTCTTCTTGTCTCAGGATCTCTCCCGTCCGTATATGC 171461
Qy      1467  CAAGGGATCCGCGCGCGCTGCTGCTCTGAGCCGCTGATCCGTA 1515

```

Db 171462 CAAGGATCCCGCGGCGCGCTGCTGCTCTGAGCGCGCTGATCGTA 171510

## RESULT 15

US-08-630-822A-61  
 ; Sequence 61, Application US/08630822A  
 ; Patent No. 5840695  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANK, GLENN R.  
 ; APPLICANT: HUNTER, SHIRLEY WU  
 ; APPLICANT: WALLENFELS, LYNDIA  
 ; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS  
 ; TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln Street, Suite 3500  
 ; CITY: Denver  
 ; STATE: Colorado  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/630,822A  
 ; FILING DATE: 11-APR-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CONNELL, GARY J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2618-17-C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 61:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2706 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 5..2706  
 ; US-08-630-822A-61

Query Match 12.8%; Score 194; DB 2; Length 2706;  
 Best Local Similarity 54.4%; Pred.No. 5.3e-54;  
 Matches 492; Conservative 0; Mismatches 385; Indels 27; Gaps 4;  
 QY 287 CAAGGACTCGAAGTCAGAAGCTTTGTAGGTGTGGTGCACCTTTGCTGAAGTGCAGGTGG 346  
 Db 78 CAGATGATTTTAATTAATAAAGTTATTGGTCGAGGACATTTGGTGAAGTACAGTTAG 137  
 QY 347 TAAGAGAGAAAGCAACCGGGACATCTATGCTATGAAGTGTGAAGAGAGGCTTTAT 406  
 Db 138 TCGCACACAAATCAACTGCACAAAGTTTGTCTATGAACGCGCTATCAAAAATTTGAAATGA 197  
 QY 407 TGGCCCGAGGAGGAGTTTCATTTTTTTAGGAAGAGCGGAACATATTATCTCGAAGCAAA 466  
 Db 198 TTAAGAGACGACACTCTGCATTTTTTTGGGAAGAAGCTCATATATGGCTCATGCAAAAT 257  
 QY 467 GCCCGTGGATCCCGAATTTACAGTAGTCCCTTCAGGACAAAAATCACCTTTTATCTGGTCA 526  
 Db 258 CAGATGGGATGTACAAATTTACATTTTGTCTTTTCAAGATCAAAAATATCTTTATATGGTCA 317  
 QY 527 TGGAAATATCAGGCTCGAGGGGACTTGTCTCACTTTTGAATAGATATGAGGACCAAGTTAG 586  
 Db 318 TGGATTATATCGCGGGGGTGACTTGGTGAGTCTTATG-----TCCGATTATGAATTC 371

QY 587 ATGAAACCTGATACAGCTTTTACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATC 646  
 Db 372 CAGAAAATATGGGCAATGTTCTATACAATGGAAGTGGTGCTAGCACCTTGATACAAATTCAC 431  
 QY 647 TGATGGGATACGTGATCGAGACATCAAGCTCGAGAACATTTCTCGTTTGACCGCACAGGAC 706  
 Db 432 CCATGGGATTTGTATACATCGTGATGTTAAACCTGATATATGCTTCTAGACAAATATGGTC 491  
 QY 707 ACATCAAGCTGCTGATTTTGGATCTCCCGGAAAATGAATTCAAACAAATGSGTAATG 766  
 Db 492 ATTTAAAGTTAGCTGACTTTTGGAACTCTGTATGAAAATGSGATACAGATGGTTTGGTAG 551  
 QY 767 CCAAACTCCCGATTGGGACCCCGAGATTACATGCTCTCGAAGTCTGACTGTGATGAACG 826  
 Db 552 CTATATATGCTGTTGGAAACGCTGATTACATTTCTCCGAAGT-----TTTGCAGTCCC 605  
 QY 827 GGGATGGAAGGACCTAGCGCTGAGCTGTGACTGGTGGTGGTGGGCGGTGATTGCGCT 886  
 Db 606 AAGGTGGTGAAGGAGTTTACGGTCTGTAATCGGATTCGATTCGTTGGTGAATTTTGTGT 665  
 QY 887 ATGAGATGATTTATGGGAGATCCCTTCGACAGAGGAACTCTGCCAGAACCTTCAATA 946  
 Db 666 ATGAATGTTATTGGGAGAAACACCTTTTATGCAGACAGTTTGGTGGAACTTACAGTA 725  
 QY 947 ACATATGAATTTCCAGCGGTTTTTGAATTTCCAGATGACCCCAAGAGTGAGCAGTGACT 1006  
 Db 726 AAATATATGGATCACAGAAACTCATTAACCTTTCTCCAGAAGTGAATAAAGCCAATATG 785  
 QY 1007 TTTCTGTATCTGATTCAAAGCTTGTGTGCGGCCAGAAAGAG-----AGACTGAAGT 1057  
 Db 786 CCGATCTTTGATACAAAGATTTTAAACAGACAGAACACAGCGTTTAGGCAGAAATGAAG 845  
 QY 1058 TTGAAGGTCTTTGTGCTGCATCCTTTCTCTCTAAAATTTGACTGGA-----ACAACTTC 1111  
 Db 846 TGAAGAAGAAATTAACAGACATCCATTTTTCATAAATGATCAATGACTTTTGGACAATTTAA 905  
 QY 1112 GTAACTCTCTCCCGCTTCTGTTCCCACTCTGAAGTCCGACGATGACACCTCCCAATTTG 1171  
 Db 906 GAGACTCTGCCCACTCTGATGCTGAGCTGAGTGTGATGATGATGATGATGATGATGATG 965  
 QY 1172 ATGA 1175  
 Db 966 ATGA 969

Search completed: November 8, 2004, 08:55:10  
 Job time : 159 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 8, 2004, 12:23:11 : Search time 39 Seconds  
(without alignments)  
845.129 Million cell updates/sec

Title: US-10-724-594-2  
Perfect score: 2602  
Sequence: 1 MLKFYKARNPLDAGAAEPI.....CSRILPSVYAKSGARGCWL 497

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap.\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2602	100.0	497	US-09-804-471A-2	Sequence 2, Appli
2	2602	100.0	497	US-10-238-709-2	Sequence 2, Appli
3	2440	93.8	1958	US-10-028-946-4	Sequence 4, Appli
4	2440	93.8	2054	US-10-028-946-2	Sequence 2, Appli
5	2271.5	87.3	494	US-09-804-471A-4	Sequence 4, Appli
6	2271.5	87.3	494	US-10-238-709-4	Sequence 2, Appli
7	1284	49.3	257	US-09-916-204-2	Sequence 2, Appli
8	1284	49.3	257	US-10-282-048-2	Sequence 2, Appli
9	1180	45.3	251	US-09-916-204-4	Sequence 4, Appli
10	1180	45.3	251	US-10-282-048-4	Sequence 4, Appli
11	1177	45.2	251	US-09-916-204-5	Sequence 5, Appli
12	1177	45.2	251	US-09-916-204-6	Sequence 6, Appli
13	1177	45.2	251	US-10-282-048-5	Sequence 5, Appli
14	1177	45.2	251	US-10-282-048-6	Sequence 6, Appli
15	865	33.2	1388	US-08-685-576-4	Sequence 4, Appli
16	865	33.2	1388	US-09-976-594-296	Sequence 296, App
17	864.5	33.2	1354	US-08-685-871-2	Sequence 2, Appli
18	860.5	33.1	1388	US-08-685-576-1	Sequence 1, Appli
19	857.5	33.0	420	US-08-685-871-58	Sequence 58, Appli
20	840.5	32.3	420	US-08-685-871-59	Sequence 59, Appli
21	828	31.8	582	US-08-422-699A-9	Sequence 9, Appli
22	828	31.8	582	US-08-422-706B-9	Sequence 9, Appli
23	790.5	30.4	900	US-08-630-822A-62	Sequence 62, Appli
24	790.5	30.4	900	US-09-005-069-62	Sequence 62, Appli
25	790.5	30.4	900	US-08-171-156A-21	Sequence 21, Appli
26	790.5	30.4	900	US-09-004-730A-21	Sequence 21, Appli
27	790.5	30.4	900	US-08-981-799A-21	Sequence 21, Appli

28	771.5	29.7	638	2	US-08-422-699A-11	Sequence 11, Appli
29	771.5	29.7	638	2	US-08-422-706B-11	Sequence 11, Appli
30	760.5	29.2	555	1	US-08-484-044-6	Sequence 6, Appli
31	711	27.3	479	3	US-09-442-100-13	Sequence 13, Appli
32	711	27.3	479	4	US-08-939-106-13	Sequence 13, Appli
33	711	27.3	479	4	US-09-442-102-13	Sequence 13, Appli
34	701	26.9	526	3	US-09-442-100-12	Sequence 12, Appli
35	701	26.9	526	4	US-08-939-106-12	Sequence 12, Appli
36	701	26.9	526	4	US-09-442-102-12	Sequence 12, Appli
37	686	26.4	719	3	US-09-588-256-2	Sequence 2, Appli
38	683	26.2	404	2	US-08-860-150-3	Sequence 3, Appli
39	683	26.2	404	3	US-09-338-132-3	Sequence 3, Appli
40	677	26.0	464	2	US-08-878-989-4	Sequence 4, Appli
41	677	26.0	464	3	US-09-272-796-4	Sequence 4, Appli
42	674.5	25.9	465	2	US-08-878-989-18	Sequence 18, Appli
43	674.5	25.9	465	2	US-08-860-150-7	Sequence 7, Appli
44	674.5	25.9	465	3	US-09-338-132-7	Sequence 7, Appli
45	674.5	25.9	465	3	US-09-272-796-18	Sequence 18, Appli

## ALIGNMENTS

### RESULT 1

US-09-804-471A-2  
; Sequence 2, Application US/09804471A  
; Patent No. 6479269  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-09-804-471A-2

Query Match	100.0%	Score	2602;	DB	4;	Length	497;
Best Local Similarity	100.0%	Pred. No.	1.4e-242;				
Matches	497;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MLKFYKARNPLDAGAAEPIANRSLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE	60				
DB	1	MLKFYKARNPLDAGAAEPIANRSLNLFQGGKPPFMTQQQMSPLSREGILDALFVLFE	60				
QY	61	ECSPALMKIKHVSFVRKYSRTIAELQLOPSAKDFVRSILVGCCHFAEVQVREKATG	120				
DB	61	ECSPALMKIKHVSFVRKYSRTIAELQLOPSAKDFVRSILVGCCHFAEVQVREKATG	120				
QY	121	DIYAKVMKKALLAQEQVSRFEERNILSRSTSPWIPQLOVAFODKXHLVLMVYQPG	180				
DB	121	DIYAKVMKKALLAQEQVSRFEERNILSRSTSPWIPQLOVAFODKXHLVLMVYQPG	180				
QY	181	DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPNILVDRTHIKLVDF	240				
DB	181	DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGYVHRDIKPNILVDRTHIKLVDF	240				
QY	241	GSAAKVNSNMVNAKPIGTDPYMAPEVLTVNMGKGTYGLDCDWSVGVYAYEMVYGR	300				
DB	241	GSAAKVNSNMVNAKPIGTDPYMAPEVLTVNMGKGTYGLDCDWSVGVYAYEMVYGR	300				
QY	301	SFPAEGTSARTNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKERLKEGGLCHPFF	360				
DB	301	SFPAEGTSARTNNIMNFORFLKFPDDPKVSSDFDLIQSLLCGQKERLKEGGLCHPFF	360				
QY	361	SKIDWNIPNSPPFVTLKSDDDTSNDFPEKNSWSSPCQLSPSFGSSEELPFVCGFS	420				
DB	361	SKIDWNIPNSPPFVTLKSDDDTSNDFPEKNSWSSPCQLSPSFGSSEELPFVCGFS	420				

Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGBELPFGVS 420  
 QY 421 YSKALGILGRSESVSGSLDSPAKTSMKELLIKSKELQDSQDKCHKVFIISAAGLLPCSR 480  
 Db 421 YSKALGILGRSESVSGSLDSPAKTSMKELLIKSKELQDSQDKCHKVFIISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGCWL 497  
 Db 481 ILPSVYAKSGARGCWL 497

RESULT 2  
 US-10-238-709-2  
 ; Sequence 2, Application US/10238709  
 ; Patent No. 6680188  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001164DIV  
 ; CURRENT APPLICATION NUMBER: US/10/238,709  
 ; CURRENT FILING DATE: 2002-09-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 497  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-10-238-709-2

Query Match 100.0%; Score 2602; DB 4; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-242;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVSRLVGCCHGFAEVQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVSRLVGCCHGFAEVQVREKATG 120  
 QY 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180  
 Db 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
 QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWSVGVIAEMYIGR 300  
 Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWSVGVIAEMYIGR 300  
 QY 301 SPFAEGTSARTFNNINMNFQFLKFPDDPKVSSDFDLIQLSCGQKERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNINMNFQFLKFPDDPKVSSDFDLIQLSCGQKERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGBELPFGVS 420  
 Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGBELPFGVS 420  
 QY 421 YSKALGILGRSESVSGSLDSPAKTSMKELLIKSKELQDSQDKCHKVFIISAAGLLPCSR 480  
 Db 421 YSKALGILGRSESVSGSLDSPAKTSMKELLIKSKELQDSQDKCHKVFIISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGCWL 497  
 Db 481 ILPSVYAKSGARGCWL 497

RESULT 3

US-10-028-946-4  
 ; Sequence 4, Application US/10028946  
 ; Patent No. 6734009  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Xuanchuan  
 ; APPLICANT: Miranda, Maricar  
 ; APPLICANT: Friddle, Carl Johan  
 ; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0289-USA  
 ; CURRENT APPLICATION NUMBER: US/10/028,946  
 ; CURRENT FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/258,335  
 ; PRIOR FILING DATE: 2000-12-27  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1958  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-028-946-4

Query Match 93.8%; Score 2440; DB 4; Length 1958;  
 Best Local Similarity 99.6%; Pred. No. 5e-226;  
 Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFTMQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVSRLVGCCHGFAEVQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVSRLVGCCHGFAEVQVREKATG 120  
 QY 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180  
 Db 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVD 240  
 QY 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWSVGVIAEMYIGR 300  
 Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLTVMGDGKGTGYGLDCDWSVGVIAEMYIGR 300  
 QY 301 SPFAEGTSARTFNNINMNFQFLKFPDDPKVSSDFDLIQLSCGQKERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNINMNFQFLKFPDDPKVSSDFDLIQLSCGQKERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGBELPFGVS 420  
 Db 361 SKIDWNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQLSPSGSGBELPFGVS 420  
 QY 421 YSKALGILGRSESVSGSLDSPAKTSMKELLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVSGSLDSPAKTSMKELLIKSKELQDSQDKCHKV 468

RESULT 4  
 US-10-028-946-2  
 ; Sequence 2, Application US/10028946  
 ; Patent No. 6734009  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Xuanchuan  
 ; APPLICANT: Miranda, Maricar  
 ; APPLICANT: Friddle, Carl Johan  
 ; TITLE OF INVENTION: No. 6734009el Human Kinases and Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0289-USA  
 ; CURRENT APPLICATION NUMBER: US/10/028,946  
 ; CURRENT FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/258,335  
 ; PRIOR FILING DATE: 2000-12-27  
 ; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 2054

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-028-946-2

Query Match

Best Local Similarity 93.8%; Score 2440; DB 4; Length 2054;

Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60

DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

QY 121 DIYAMKMKKALLAQEQVSFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180

DB 121 DIYAMKMKKALLAQEQVSFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180

QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPNILVDRTHIKLVDF 240

DB 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDMSVGVYAYEMIYGR 300

DB 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDMSVGVYAYEMIYGR 300

QY 301 SPFAEGTSARTFNINMFORFLKPPDPKVSSDFLDLIQSLCCGKERLKFEGLCCHPFF 360

DB 301 SPFAEGTSARTFNINMFORFLKPPDPKVSSDFLDLIQSLCCGKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420

DB 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420

QY 421 YSKALGILGRESVVSGLDSPAKTSMEKLLIKSKELQSDQKCHKVPIAAGLLPCSR 480

DB 421 YSKALGILGRESVVSGLDSPAKTSMEKLLIKSKELQSDQKCHKVPIAAGLLPCSR 480

RESULT 5

US-09-804-471A-4

; Sequence 4, Application US/09804471A

; Patent No. 6479269

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001164

; CURRENT APPLICATION NUMBER: US/09/804,471A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 494

; TYPE: PRT

; ORGANISM: Mus Musculus

US-09-804-471A-4

Query Match

Best Local Similarity 87.3%; Score 2271.5; DB 4; Length 494;

Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60

DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

QY 121 DIYAMKMKKALLAQEQVSFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180

DB 121 DIYAMKMKKALLAQEQVSFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180

QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPNILVDRTHIKLVDF 240

DB 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDMSVGVYAYEMIYGR 300

DB 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDMSVGVYAYEMIYGR 300

QY 301 SPFAEGTSARTFNINMFORFLKPPDPKVSSDFLDLIQSLCCGKERLKFEGLCCHPFF 360

DB 301 SPFAEGTSARTFNINMFORFLKPPDPKVSSDFLDLIQSLCCGKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420

DB 361 SKIDMNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSPCQLSPSGFSGEELPFVGF 420

QY 421 YSKALGILGRESVVSGLDSPAKTSMEKLLIKSKELQSDQKCHKVPIAAGLLPCSR 480

DB 421 YSKALGILGRESVVSGLDSPAKTSMEKLLIKSKELQSDQKCHKVPIAAGLLPCSR 480

QY 481 ILPSVYAKSGARGRC 495

DB 481 ILPSVYAKSGARGRC 495

RESULT 6

US-10-238-709-4

; Sequence 4, Application US/10238709

; Patent No. 6680188

; GENERAL INFORMATION:

; APPLICANT: WEBSTER, Marion et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001164DIV

; CURRENT APPLICATION NUMBER: US/10/238,709

; CURRENT FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 494

; TYPE: PRT

; ORGANISM: Mus Musculus

US-10-238-709-4

Query Match

Best Local Similarity 87.3%; Score 2271.5; DB 4; Length 494;

Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60

DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60

QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120

QY 121 DIYAMKMKKALLAQEQVSFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180

DB 121 DIYAMKMKKALLAQEQVSFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG 180

QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPNILVDRTHIKLVDF 240

DB 181 DLLSLNRYEDQDLENLIQFYLAELILAVHSVHMGVYVHRDIKPNILVDRTHIKLVDF 240

QY 241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVNMGDGKGTGYGLDCDMSVGVYAYEMIYGR 300

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Db 241 GSAKMSNK-VDAKLPIGTPDYMAPEVLTVMNEEDRRGTGLDCLDWSVGVWAYENVYCK 299
Qy 301 SPBAEGTSATFNINMFORFLKPPDDPKVSSDFLDLIQSLICGOKERLKFEGLCCHPEF 360
Db 300 TPTEGTSATFNINMFORFLKPPDDPKVSSDFLDLIQSLICGOKERLKFEGLCCHPEF 359
Qy 361 SKIDWNIRNSPPFPVTLKASDDDTNFDPEKNSVSSSPCOLSPSGFSGBELPVGFS 420
Db 360 ARTDWNIRNSPPFPVTLKASDDDTNFDPEKNSWAFILCVPAEPLAFSGEELPVGFS 419
Qy 421 YSRALGILGRSESVVSGLDSPAKTSMEKLLIKSELQDSQDKCHKVFIISAAGLLPCSR 480
Db 420 YSRALGILGRSESVVSGLDSPAKTSMEKLLIKSELQDSQDKCHKVFIISAAGLLPCSR 479
Qy 481 ILPSVYAKGSARGRC 495
Db 480 ILQSIYAEAGSAGGHC 494

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RESULT 7
US-09-916-204-2
; Sequence 2, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
; US-09-916-204-2

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Query Match 49.3%; Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%; Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSRREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSRREGILDALFVLFE 60
Qy 61 ECSQPALMKIKHVSNFVRKYSYDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSYDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPQLOQYAFQDKNHLVLYMEYOPGG 180
Db 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPQLOQYAFQDKNHLVLYMEYOPGG 180
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVYHVDIKPENILVDRTHGHIKLVD 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVYHVDIKPENILVDRTHGHIKLVD 240
Qy 241 GSAAKMSNRKV 252
Db 241 GSAAKMSNRKV 252

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RESULT 8
US-10-282-048-2
; Sequence 2, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
; US-10-282-048-2

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Query Match 49.3%; Score 1284; DB 4; Length 257;
Best Local Similarity 99.6%; Pred. No. 1.1e-115;
Matches 251; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSRREGILDALFVLFE 60
Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTQQQMSPLSRREGILDALFVLFE 60
Qy 61 ECSQPALMKIKHVSNFVRKYSYDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSYDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPQLOQYAFQDKNHLVLYMEYOPGG 180
Db 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPQLOQYAFQDKNHLVLYMEYOPGG 180
Qy 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVYHVDIKPENILVDRTHGHIKLVD 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVYHVDIKPENILVDRTHGHIKLVD 240
Qy 241 GSAAKMSNRKV 252
Db 241 GSAAKMSNRKV 252

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RESULT 9
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-916-204-4

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Best Local Similarity 90.4%; Pred. No. 1.2e-105;
Matches 227; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

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Qy 61 ECSQPALMKIKHVSNFVRKYSYDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSYDTIAELQELQPSAKDFEVSRLVGCCHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKALLAQOVSFFEEERNILSRSTSPWIPQLOQYAFQDKNHLVLYMEYOPGG 180
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; Sequence 5, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-282-048-5

Query Match          45.2%; Score 1177; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.3e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

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DB 1 MLKFKYGVRRPPEASASEPIASRASRLNLFQGGKPPFTMQOQMSPLSRREGILDALFALPE 60
QY 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSPFEEERNILSRSTSPWIPQOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DVYAMKMKKALLAQEQVSPFEEERNILSRSTSPWIPQOLQYAFQDKNHLVLMVEYQPGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVHMGVYVHRDIPENILVDRTGHIKLVDF 240
DB 181 DFLSLNRYEDQDENLIQFYLAELILAVSHVHMGVYVHRDIPENILVDRTGHIKLVDF 240
QY 241 GSAAKMNSNM 251
DB 241 GSAAKMNSNKV 251

RESULT 14
US-10-282-048-6
; Sequence 6, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-282-048-6

Query Match          45.2%; Score 1177; DB 4; Length 251;
Best Local Similarity 90.0%; Pred. No. 2.3e-105;
Matches 226; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

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DB 1 MLKFKYGVRRPPEASASEPIASRASRLNLFQGGKPPFTMQOQMSPLSRREGILDALFALPE 60
QY 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
DB 61 ECSOPALMKIKHVSFVRYKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVSPFEEERNILSRSTSPWIPQOLQYAFQDKNHLVLMVEYQPGG 180
DB 121 DVYAMKMKKALLAQEQVSPFEEERNILSRSTSPWIPQOLQYAFQDKNHLVLMVEYQPGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVHMGVYVHRDIPENILVDRTGHIKLVDF 240
DB 181 DFLSLNRYEDQDENLIQFYLAELILAVSHVHMGVYVHRDIPENILVDRTGHIKLVDF 240
QY 241 GSAAKMNSNM 251
DB 241 GSAAKMNSNKV 251

RESULT 15
US-08-685-576-4
; Sequence 4, Application US/08685576
; Patent No. 5906819
; GENERAL INFORMATION:
; APPLICANT: Kaibuchi, Kozi
; APPLICANT: Iwamatsu, Akihiro
; APPLICANT: Nakano, Takeshi
; APPLICANT: Ito, Masaaki
; APPLICANT: Takahashi, No. 5906819uaki
; TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/685,576
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-325129
; FILING DATE: 20-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-17150
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-131206
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16897/843
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1388 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-685-576-4

Query Match          33.2%; Score 865; DB 2; Length 1388;
Best Local Similarity 40.1%; Pred. No. 4.2e-74;
Matches 181; Conservative 97; Mismatches 141; Indels 32; Gaps 10;

QY 24 ASRLNLFQGGKPPFTMQOQMSPLSRREGILDALFVLFECSOPALMKIKHVSFVRYKSDT 83

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Qy 84 IAELOELQPSAKOPEVRSVLCGCHFAEVOVVRKATGDIYAMKVMKKALLAQEQVSPFE 143  
Db 79 VKIKIGLQMAEDYDVVKVIGRGAFGEVQLVRHKASQKVYAMKLLSKFEMIKRSDSAFPW 138  
Qy 144 EERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGGDLISLNRXYEDQIDENLIQFYLA 203  
Db 139 EERDIFAFANSPPWVQLFYAFQDDRYLYMYWYMPGGDLVNLMSNYD--VPEKWKAFYTA 196  
Qy 204 ELILAVESVHLMGVVHRDIKPENILVDRTGHIKLVDPGSAKONSKNKNVNAKLPIGTPDY 263  
Db 197 EVLALDAIHSMGLIHRDVKPDNLLDKHGHLKLADFGTCMKVDETCMVHCHDFAVGTPDY 256  
Qy 264 MAPEVLTVMNGDGKGTGLDCDWMVSGVIAIYEMVGRSPFAEGTSARTFNINMNFORFLK 323  
Db 257 ISPEVLKSQGD--GFYGRCDWMVSGVFLYEMLVGDTFPYADSLVGYTSKINDHKNSLC 314  
Qy 324 PPDDPKVSDFLDLIOQLCGQKRLKPEG---LCCHPFF--SKIDWNINRNSPPFPVPT 378  
Db 315 FPEDAEISKHAKNLICAFLTDRVRLGRNGVEBIRQHPFFKNDQWHWDNIRETAAPVPE 374  
Qy 379 LKSDDDTSNFEDEKNSM-VSSPCQLSPSGRSGEELPFVGFYSYKALGILGRSESVWSG 437  
Db 375 LSSDIDSSNFDDIEDDKGDVETFPi---PKAFVGNQLPFIgfTYRENLLS----- 423  
Qy 438 LDSPA--KTSSMEKKLLIKSKELQDSQDKCH 466  
Db 424 -DSPSCRENDSIQSR---KNEESQEIQKLY 450

Search completed: November 8, 2004, 12:33:04  
Job time : 40 secs

**It is Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 12:31:42 ; Search time 141 Seconds  
(without alignments)  
1245.059 Million cell updates/sec

Title: US-10-724-594-2  
Perfect score: 2602  
Sequence: 1 MLKFKYARNPLDAGAAEPI.....CSRILPSVYAKSARGRWL 497

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/protdata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/protdata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/protdata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/protdata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/protdata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/protdata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2602	100.0	497	9	US-09-804-471A-2
2	2602	100.0	497	14	US-10-238-709-2
3	2602	100.0	497	15	US-10-724-594-2
4	2589	99.5	497	15	US-10-311-034-7
5	2440	93.8	623	15	US-10-262-511-4
6	2440	93.8	1958	13	US-10-028-946-4
7	2440	93.8	1958	17	US-10-791-666-4
8	2440	93.8	2054	13	US-10-028-946-2
9	2440	93.8	2054	15	US-10-415-011-21
10	2440	93.8	2054	17	US-10-791-666-2
11	2430	93.4	2053	13	US-10-017-216-2
12	2430	93.4	2053	14	US-10-325-430-12
13	2430	93.4	2053	17	US-10-757-262-52

14	2418.5	92.9	2055	17	US-10-618-941-67	Sequence 67, Appl
15	2412.5	92.7	2053	11	US-09-964-956-11	Sequence 11, Appl
16	2412.5	92.7	2053	15	US-10-262-511-2	Sequence 2, Appl
17	2412.5	92.7	2066	11	US-09-964-956-9	Sequence 9, Appl
18	2412.5	92.7	2066	15	US-10-262-511-14	Sequence 14, Appl
19	2271.5	87.3	494	9	US-09-804-471A-4	Sequence 4, Appl
20	2271.5	87.3	494	14	US-10-238-709-4	Sequence 4, Appl
21	2271.5	87.3	494	15	US-10-724-594-4	Sequence 4, Appl
22	2172.5	83.5	2055	13	US-10-017-216-4	Sequence 2, Appl
23	1652	63.5	319	14	US-10-412-897-2	Sequence 2, Appl
24	1284	49.3	257	14	US-10-282-048-2	Sequence 2, Appl
25	1180	45.3	251	14	US-10-282-048-4	Sequence 4, Appl
26	1177	45.2	251	14	US-10-282-048-5	Sequence 5, Appl
27	932.5	35.8	1565	16	US-10-702-496-2	Sequence 6, Appl
28	929	35.7	475	15	US-10-415-011-2	Sequence 2, Appl
29	929	35.7	1572	14	US-10-333-314-20	Sequence 20, Appl
30	929	35.7	1572	17	US-10-618-941-68	Sequence 68, Appl
31	929	34.2	1719	14	US-10-369-493-6347	Sequence 6347, Ap
32	908.5	34.9	1548	14	US-10-012-697-1540	Sequence 219, App
33	896.5	34.5	1000	14	US-09-771-161A-219	Sequence 220, App
34	896.5	34.5	1711	9	US-09-771-161A-220	Sequence 10, Appl
35	896.5	34.5	1711	15	US-10-399-225-10	Sequence 228, App
36	896.5	34.2	496	9	US-09-771-161A-228	Sequence 2, Appl
37	891	34.2	1719	14	US-10-288-798-2	Sequence 2, Appl
38	891	34.2	1719	15	US-10-362-892-2	Sequence 19, Appl
39	891	34.2	1770	15	US-10-433-794-19	Sequence 4, Appl
40	891	34.2	1572	16	US-10-702-496-4	Sequence 102, App
41	890	34.2	1664	15	US-10-210-130-102	Sequence 100, App
42	882.5	33.9	1738	15	US-10-210-130-100	Sequence 671, App
43	882.5	33.9	573	9	US-09-764-868-671	Sequence 1205, Ap
44	877.5	33.7	573	11	US-09-764-875-1205	
45	877.5	33.7	573	11	US-09-764-875-1205	

ALIGNMENTS

RESULT 1

US-09-804-471A-2  
; Sequence 2, Application US/09804471A  
; Patent No. US20020132322A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Human  
US-09-804-471A-2

Query Match	100.0%	Score 2602;	DB 9;	Length 497;
Best Local Similarity	100.0%	Pred. No. 1.9e-184;		
Matches	497;	Conservative	0;	Mismatches
		Indels	0;	Gaps
				0;
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Db	1	MLKFKYARNPLDAGAAEPIANRASRLNLFQGGKPPFTQOQMSPLSREGILDALFVLFE	60	
Qy	61	ECSQALMKIKHVSNFVKYSDTIAELQLOPSAKDFEVRSLVGGHFAEVQVVRKATG	120	
Db	61	ECSQALMKIKHVSNFVKYSDTIAELQLOPSAKDFEVRSLVGGHFAEVQVVRKATG	120	
Qy	121	DIYAMVNMKKALLAQEQVSFFEBERNILSRSTSPWIPQLOQYAFQDNKHLVLYMEYOPGG	180	
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 QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSFNDEPEKNSWVSSSPCQLSPSGSGSEELPFVGF 420  
 DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSFNDEPEKNSWVSSSPCQLSPSGSGSEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGRCWL 497  
 DB 481 ILPSVYAKSGARGRCWL 497

RESULT 2  
 US-10-238-709-2  
 ; Sequence 2, Application US/10238709  
 ; Publication No. US20030022340A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; FILE REFERENCE: CL001164DIV  
 ; CURRENT APPLICATION NUMBER: US/10/238,709  
 ; CURRENT FILING DATE: 2002-09-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 497  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-10-238-709-2

Query Match 100.0%; Score 2602; DB 14; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-184;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQOKPPFMTQQQMSPLSREGILDALFVLE 60  
 DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQOKPPFMTQQQMSPLSREGILDALFVLE 60  
 QY 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
 DB 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
 QY 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180  
 DB 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMMYGR 300  
 DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMMYGR 300  
 QY 301 SPFAEGTSARTFNNINMNFORFLKFPDDPKVSSDFDLQSLLCGOKERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNNINMNFORFLKFPDDPKVSSDFDLQSLLCGOKERLKFEGLCCHPFF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSFNDEPEKNSWVSSSPCQLSPSGSGSEELPFVGF 420  
 DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSFNDEPEKNSWVSSSPCQLSPSGSGSEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGRCWL 497  
 DB 481 ILPSVYAKSGARGRCWL 497

RESULT 3  
 US-10-724-594-2  
 ; Sequence 2, Application US/10724594  
 ; Publication No. US20040091993A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; FILE REFERENCE: CL001164DIV II  
 ; CURRENT APPLICATION NUMBER: US/10/724,594  
 ; CURRENT FILING DATE: 2003-12-02  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 497  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-724-594-2

Query Match 100.0%; Score 2602; DB 15; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-184;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQOKPPFMTQQQMSPLSREGILDALFVLE 60  
 DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQOKPPFMTQQQMSPLSREGILDALFVLE 60  
 QY 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
 DB 61 ECSQPALMKIKHVSFNVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120  
 QY 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180  
 DB 121 DIYAMKMKKALLAQEQSVFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYQPG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMMYGR 300  
 DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVNMGDKGTGYGLDCDWSVGVYAYEMMYGR 300  
 QY 301 SPFAEGTSARTFNNINMNFORFLKFPDDPKVSSDFDLQSLLCGOKERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNNINMNFORFLKFPDDPKVSSDFDLQSLLCGOKERLKFEGLCCHPFF 360  
 QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSFNDEPEKNSWVSSSPCQLSPSGSGSEELPFVGF 420  
 DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSFNDEPEKNSWVSSSPCQLSPSGSGSEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGRCWL 497  
 DB 481 ILPSVYAKSGARGRCWL 497

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RESULT 4
US-10-311-034-7
; Sequence 7, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROMSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAPALIA, Apnil
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: KHO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIFON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: FI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,457; 60/215,651; 60/216,605; 60/218,372; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1
US-10-311-034-7

Query Match          99.5%; Score 2589; DB 15; Length 497;
Best Local Similarity 99.6%; Pred. No. 1.8e-183;
Matches 495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKFYKARNPLDAGAAEPIANRSLNLFQCKPPFMTQQQMSPLRSRGILDALFVLPE 60
Db 1 MLKFYKARNPLDAGAAEPIASRSLNLFQCKPPFMTQQQMSPLRSRGILDALFVLPE 60
QY 61 ECSOPALMKIKHVSFVRKYSDTIAELQLOPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 61 ECSOPALMKIKHVSFVRKYSDTIAELQLOPSAKDFEVRSLVGCCHFAEVQVREKATG 120

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QY 121 DIYAKWKKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKXNHLVLYMEYOPGG 180
Db 121 DIYAKWKKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKXNHLVLYMEYOPGG 180
QY 181 DLLSLNRYEDQLDENITQFYLAELIILAVHSVHLMGYVHRDIKPENILVDRTHIKLVDF 240
Db 181 DLLSLNRYEDQLDENITQFYLAELIILAVHSVHLMGYVHRDIKPENILVDRTHIKLVDF 240
QY 241 GSAAKMSNKKVNAKLPIGTPDYVAPEVLTVNMGDGKGTGCLDCDMSVGVIAIEMTYGR 300
Db 241 GSAAKMSNKKVNAKLPIGTPDYVAPEVLTVNMGDGKGTGCLDCDMSVGVIAIEMTYGR 300
QY 301 SPFAEGTSARTFNIMNFQRELKFPDPPKVSDDFLDIQSLCCQKERLKEGCLCHPFF 360
Db 301 SPFAEGTSARTFNIMNFQRELKFPDPPKVSDDFLDIQSLCCQKERLKEGCLCHPFF 360
QY 361 SKIDWNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420
Db 361 SKIDWNNIRNSPPFPVPTLKSDDTSNFDPEKNSWSSSPCQLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLIIKSKELOQSDQKCHKVFIISAAGLLPCSR 480
Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLIIKSKELOQSDQKCHKVFIISAAGLLPCSR 480
QY 481 ILPSVYAKGSARGRCWL 497
Db 481 ILPSVYAKGSARGRCWL 497

RESULT 5
US-10-262-511-4
; Sequence 4, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Willet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09

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; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-511-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 15; Length 623;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASLNLFQCKPFPMTQQQMSPLSRGILDALFVLPE 60
Db 5 MLKFKYGARNPLDAGAAEPIASRASLNLFQCKPFPMTQQQMSPLSRGILDALFVLPE 64
QY 61 ECSQPALMKIKHVSNFVRKYSOTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 65 ECSQPALMKIKHVSNFVRKYSOTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 124
QY 121 DIYAMKMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQGG 180
Db 125 DIYAMKMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQGG 184
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
Db 185 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 244
QY 241 GSAAKMNSNMVNAKLPITGPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMMYGR 300
Db 245 GSAAKMNSNMVNAKLPITGPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMMYGR 304
QY 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLIQSLCCGOKERLKFEGLCCHPFF 360
Db 305 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLIQSLCCGOKERLKFEGLCCHPFF 364
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNDFEPEKNWSVSSPCQLSPSGFSGBELPFVGF 420
Db 365 SKIDMNNIRNSPPFPVPTLKSDDDTSNDFEPEKNWSVSSPCQLSPSGFSGBELPFVGF 424
QY 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKV 468
Db 425 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKM 472

RESULT 6
US-10-028-946-4
; Sequence 4, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-791-666-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 17; Length 1958;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-028-946-4

Query Match
Best Local Similarity 93.8%; Score 2440; DB 13; Length 1958;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASLNLFQCKPFPMTQQQMSPLSRGILDALFVLPE 60
Db 1 MLKFKYGARNPLDAGAAEPIASRASLNLFQCKPFPMTQQQMSPLSRGILDALFVLPE 60
QY 61 ECSQPALMKIKHVSNFVRKYSOTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 61 ECSQPALMKIKHVSNFVRKYSOTIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
QY 121 DIYAMKMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQGG 180
Db 121 DIYAMKMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQGG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240
QY 241 GSAAKMNSNMVNAKLPITGPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMMYGR 300
Db 241 GSAAKMNSNMVNAKLPITGPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMMYGR 300
QY 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLIQSLCCGOKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTNNINMFORFLKFPDDPKVSSDFLDLIQSLCCGOKERLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNDFEPEKNWSVSSPCQLSPSGFSGBELPFVGF 420
Db 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNDFEPEKNWSVSSPCQLSPSGFSGBELPFVGF 420
QY 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKV 468
Db 421 YSKALGILGRSSVSGLDSPAKTSSMEKKLLIKSKELQDSODKCHKM 468

RESULT 7
US-10-791-666-4
; Sequence 4, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-791-666-4

Query Match
Best Local Similarity 99.8%; Score 2440; DB 17; Length 1958;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```



```

QY 1 MLKFKYGARNPLDAGAAEPTIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLE 60
Db 1 MLKFKYGARNPLDAGAAEPTIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSFNRKYSYDIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 61 ECSQPALMKIKHVSFNRKYSYDIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPG 180
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240
Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240
QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDQCDWMSVGVIAEYMIYGR 300
Db 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDQCDWMSVGVIAEYMIYGR 300
QY 301 SPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLGCGQKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLGCGQKERLKFEGLCCHPFF 360
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCOLSPSGFSGEELPFVGF 420
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCOLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV 468

```

RESULT 8

```

US-10-028-946-2
; Sequence 2, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fridge, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

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```

Query Match 93.8%; Score 2440; DB 13; Length 2054;
Best Local Similarity 99.6%; Pred. No. 1.1e-171;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MLKFKYGARNPLDAGAAEPTIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLE 60
Db 1 MLKFKYGARNPLDAGAAEPTIANRASRLNLFQCKPFPMTQQQMSPLSRGILDALFVLE 60
QY 61 ECSQPALMKIKHVSFNRKYSYDIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
Db 61 ECSQPALMKIKHVSFNRKYSYDIAELQELQPSAKDFEVRSLVGCCHFAEVQVREKATG 120
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPG 180
Db 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPG 180
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240

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Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHIKLVDF 240
QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDQCDWMSVGVIAEYMIYGR 300
Db 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDQCDWMSVGVIAEYMIYGR 300
QY 301 SPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLGCGQKERLKFEGLCCHPFF 360
Db 301 SPFAEGTSARTFNINMFQFLKFPDDPKVSSDFLDLIQSLGCGQKERLKFEGLCCHPFF 360
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCOLSPSGFSGEELPFVGF 420
Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCOLSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV 468
Db 421 YSKALGILGRSESVVSGLDSPAKTSMEKKLLIKSKELQDSQDKCHKV 468

```

RESULT 9

```

US-10-415-011-21
; Sequence 21, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01

```

; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PERL Program  
; SEQ ID NO 21  
; LENGTH: 2054  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CD1  
US-10-415-011-21

Query Match 93.8%; Score 2440; DB 15; Length 2054;

Best Local Similarity 99.6%; Pred. No. 1.1e-171;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFMTQQQMSPLSRGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQCKPPFMTQQQMSPLSRGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEVOVVRKATG 120  
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEVOVVRKATG 120  
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
QY 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMYYGR 300  
DB 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMYYGR 300  
QY 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLQSLCQGERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLQSLCQGERLKFEGLCCHPFF 360  
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNSWSSPCQLSPGSGEELPFVGF 420  
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNSWSSPCQLSPGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468  
DB 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468

## RESULT 10

US-10-791-666-2  
; Sequence 2, Application US/10791666  
; Publication No. US20040209297A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Kuanchuan  
; APPLICANT: Miranda, Maricar  
; APPLICANT: Fiddler, Carl Johan  
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0289-USA  
; CURRENT APPLICATION NUMBER: US/10/791,666  
; PRIOR FILING DATE: 2004-03-02  
; PRIOR APPLICATION NUMBER: US/10/028,946  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/258,335  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 2054  
; TYPE: PRF  
; ORGANISM: homo sapiens  
US-10-791-666-2

Query Match

93.8%; Score 2440; DB 17; Length 2054;

Best Local Similarity 99.6%; Pred. No. 1.1e-171;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFMTQQQMSPLSRGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQCKPPFMTQQQMSPLSRGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEVOVVRKATG 120  
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEVOVVRKATG 120  
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
QY 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPNILVDRTHIKLVDF 240  
QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMYYGR 300  
DB 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDWMSVGVIAEMYYGR 300  
QY 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLQSLCQGERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFDLQSLCQGERLKFEGLCCHPFF 360  
QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNSWSSPCQLSPGSGEELPFVGF 420  
DB 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFEPEKNSWSSPCQLSPGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468  
DB 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468

## RESULT 11

US-10-017-216-2  
; Sequence 2, Application US/10017216  
; Publication No. US20020160483A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPILLER-LIBERMANN, Rosana  
; TITLE OF INVENTION: 13245, A No. US20020160483A1 Human Myotonic Dystrophy Type Prote  
; FILE REFERENCE: 10147-57U1  
; CURRENT APPLICATION NUMBER: US/10/017,216  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/242,429  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2053  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-017-216-2

Query Match

93.4%; Score 2430; DB 13; Length 2053;

Best Local Similarity 99.1%; Pred. No. 6.1e-171;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQCKPPFMTQQQMSPLSRGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQCKPPFMTQQQMSPLSRGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEVOVVRKATG 120  
DB 61 ECSQPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEVOVVRKATG 120  
QY 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
DB 121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180

QY 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVLMGVYHRDIKPENILVDRTHIKLVDP 240  
DB 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVLMGVYHRDIKPENILVDRTHIKLVDP 240  
QY 241 GSAKXNSNKNVNAKLPIGTFDYMABEVLVWNGDGKGTGYGLDCDMSVGVIAEMMYGR 300  
DB 241 GSAKXNSNKNVNAKLPIGTFDYMABEVLVWNGDGKGTGYGLDCDMSVGVIAEMMYGR 300  
QY 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFLDLIQSLCCGQERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFLDLIQSLCCGQERLKFEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
DB 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
RESULT 12  
US-10-325-430-12  
; Sequence 12, Application US/10325430  
; Publication No. US20030135325A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; FILE REFERENCE: 32838,336 and 52908  
; CURRENT APPLICATION NUMBER: US/10325,430  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-325-430-12  
Query Match 93.4%; Score 2430; DB 14; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 6.1e-171;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTWQQMSPLSREGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTWQQMSPLSREGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120  
DB 61 ECSQPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180  
DB 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180  
QY 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVLMGVYHRDIKPENILVDRTHIKLVDP 240  
DB 181 DLLSLNRYEDQDLDENLIQFYLAELILAVSHVLMGVYHRDIKPENILVDRTHIKLVDP 240  
QY 241 GSAKXNSNKNVNAKLPIGTFDYMABEVLVWNGDGKGTGYGLDCDMSVGVIAEMMYGR 300  
DB 241 GSAKXNSNKNVNAKLPIGTFDYMABEVLVWNGDGKGTGYGLDCDMSVGVIAEMMYGR 300  
QY 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFLDLIQSLCCGQERLKFEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFLDLIQSLCCGQERLKFEGLCCHPFF 360

QY 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
DB 361 SKIDWNIRNSPPFPVPTLKSDDTSNFDPEKNSWVSSPCQLSPSGSGEELPFVGF 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
RESULT 13  
US-10-757-262-52  
; Sequence 52, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 3395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; FILE REFERENCE: MPI03-007P1RNMNM  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742  
; PRIOR FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/488,529  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 60/491,156  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 60/499,594  
; PRIOR FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US 60/506,332  
; PRIOR FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-757-262-52  
Query Match 93.4%; Score 2430; DB 17; Length 2053;  
Best Local Similarity 99.1%; Pred. No. 6.1e-171;  
Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTWQQMSPLSREGILDALFVLFE 60  
DB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGKPPFTWQQMSPLSREGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120  
DB 61 ECSQPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180  
DB 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPQLOYAFQDKNHLYLVMEYOPGG 180

QY 181 DLLSLNRYEDQDENLQFYLAELILAVHVELMGVYVHRDIPKENILVDRTHGIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLQFYLAELILAVHVELMGVYVHRDIPKENILVDRTHGIKLVDF 240  
 QY 241 GSAKQNSNMVNAKLPICGTPDYMAPEVLTVNMGDKGTYGLDCDWSVGVYAYEMIYGR 300  
 Db 241 GSAKQNSNMVNAKLPICGTPDYMAPEVLTVNMGDKGTYGLDCDWSVGVYAYEMIYGR 300  
 QY 301 SPFAEGTSARTFNNINFORFLKFPDDPKVSDDFDLQSLICGQKERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNINFORFLKFPDDPKVSDDFDLQSLICGQKERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPQQLSPSGFSGEELPFVGF 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPQQLSPSGFSGEELPFVGF 420  
 QY 421 YSKALGILGRSBSVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSBSVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468

RESULT 14

US-10-618-941-67

; Sequence 67, Application US/10618941

; Publication No. US20040197792A1

; GENERAL INFORMATION:

; APPLICANT: WHITE, DAVID

; APPLICANT: MANNING, GERARD

; APPLICANT: CAENEPEEL, SEAN

; TITLE OF INVENTION: NOVEL KINASES

; FILE REFERENCE: 034536-0321

; CURRENT APPLICATION NUMBER: US/10/618,941

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: 60/395,632

; PRIOR FILING DATE: 2002-07-15

; NUMBER OF SEQ ID NOS: 143

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 67

; LENGTH: 2055

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-618-941-67

Query Match 92.9%; Score 2418.5; DB 17; Length 2055;

Best Local Similarity 98.9%; Pred. No. 4.4e-170;

Matches 464; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 MLKFKYGARNPLDAGAAEPIANRSLNLPFGCKPFPFTQQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRSLNLPFGCKPFPFTQQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSOPALMKIKHVSNNVRK-YSDTIAELQLOPSAKDFEVRSLVCGHFAEVQVVRKAT 119  
 Db 61 ECSOPALMKIKHVSNNVRK-YSDTIAELQLOPSAKDFEVRSLVCGHFAEVQVVRKAT 120  
 QY 120 GDIYAMVKKXALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVYVMEYQPG 179  
 Db 120 GDIYAMVKKXALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVYVMEYQPG 180  
 QY 180 GDLISLNEYEQOLDENLQFYLAELILAVHVELMGVYVHRDIPKENILVDRTHGIKLV 239  
 Db 180 GDLISLNEYEQOLDENLQFYLAELILAVHVELMGVYVHRDIPKENILVDRTHGIKLV 240  
 QY 240 FGSAAQNSNMVNAKLPICGTPDYMAPEVLTVNMGDKGTYGLDCDWSVGVYAYEMIY 299  
 Db 240 FGSAAQNSNMVNAKLPICGTPDYMAPEVLTVNMGDKGTYGLDCDWSVGVYAYEMIY 300  
 QY 300 RSFPFAEGTSARTFNNINFORFLKFPDDPKVSDDFDLQSLICGQKERLKFEGLCCHPFF 359  
 Db 300 RSFPFAEGTSARTFNNINFORFLKFPDDPKVSDDFDLQSLICGQKERLKFEGLCCHPFF 360  
 QY 360 FSKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPQQLSPSGFSGEELPFVGF 419

Db 361 FSKIDWNIRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPQQLSPSGFSGEELPFVGF 420  
 QY 420 SYSKALGILGRSBSVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 468  
 Db 421 SYSKALGILGRSBSVSGLDSPAKTSMKKLLIKSKELQDSQDKCHKV 469

RESULT 15

US-09-964-956-11

; Sequence 11, Application US/09964956

; Publication No. US20040043926A1

; GENERAL INFORMATION:

; APPLICANT: Gerlach, Valerie L

; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glennda

; APPLICANT: Millet, Isabelle

; APPLICANT: Stone, David

; APPLICANT: Gunther, Erik

; APPLICANT: Ellerman, Karen

; APPLICANT: Grosse, William M

; APPLICANT: Alsobrook II, John P

; APPLICANT: Lepley, Denise M

; APPLICANT: Burgess, Catherine E

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Leach, Martin D

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20040043926A1

; FILE REFERENCE: 21402-124

; CURRENT APPLICATION NUMBER: US/09/964,956

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 60/235,631

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/235,633

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/235,808

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/236,064

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/236,065

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/236,066

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/236,135

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 60/237,434

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/238,321

; PRIOR FILING DATE: 2000-10-05

; PRIOR APPLICATION NUMBER: 60/238,399

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/238,396

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/276,667

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/294,823

; PRIOR FILING DATE: 2001-05-31

; PRIOR APPLICATION NUMBER: 60/304,868

; PRIOR FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 2053

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-964-956-11

Query Match 92.7%; Score 2412.5; DB 11; Length 2053;

Best Local Similarity 98.9%; Pred. No. 1.2e-169;

Matches 463; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy	1	MLKFKYCARNPLDAGAAEPIANFASRLNLFQCKPPEMTQOQMSPLSREGIILDALFVLE	60
Db	1	MLKFKYCARNPLDAGAAEPIASRLNLFQCKPPEMTQOQMSPLSREGIILDALFVLE	60
Qy	61	ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG	120
Db	61	ECSQPALMKIKHVSNFVRKSDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG	120
Qy	121	DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG	180
Db	121	DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPG	180
Qy	181	DLISLLNRYEDQDENLIQFYLAELILAVHSVHMGVVRDVKPENILVDRTHIKLVDF	240
Db	181	DLISLLNRYEDQDENLIQFYLAELILAVHSVHMGVVRDVKPENILVDRTHIKLVDF	240
Qy	241	GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMVSGVIAYEMIYGR	300
Db	241	GSAAKMNSNK-VNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWMVSGVIAYEMIYGR	299
Qy	301	SPEAGTSARTFNINNFQFLKFPDDPKVSSDFDLIOSLLCGQKERLKFGLCCHPFF	360
Db	300	SPEAGTSARTFNINNFQFLKFPDDPKVSSDFDLIOSLLCGQKERLKFGLCCHPFF	359
Qy	361	SKIDWNIRNSPPFPVPTLKSDDTNSFDEPEKNSWSSPCQLSPSPGSGEELPFVGFS	420
Db	360	SKIDWNIRNAPFPFPVPTLKSDDTNSFDEPEKNSWSSPCQLSPSPGSGEELPFVGFS	419
Qy	421	YSKALGILGRSESVVSGLDSPAKTSSMEKKLIIKSKELQDSQDKCHKV	468
Db	420	YSKALGILGRSESVVSGLDSPAKTSSMEKKLIIKSKELQDSQDKCHKM	467

Search completed: November 8, 2004, 12:43:48  
 Job time : 144 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 07:38:21 ; Search time 774 Seconds  
(without alignments)  
10538.677 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1 999gaatgttgaaagttcaa.....tctgagccgcctgataccgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 18: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:
- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:
- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1515	100.0	1515	US-09-804-471A-1	Sequence 1, Appli
2	1515	100.0	1515	US-10-238-709-1	Sequence 1, Appli
3	1515	100.0	1515	US-10-724-594-1	Sequence 1, Appli
4	1510.2	99.7	2056	US-10-311-034-33	Sequence 33, Appl
5	1404.2	92.7	6298	US-10-415-011-43	Sequence 43, Appl
6	1398.2	92.3	1870	US-10-262-511-3	Sequence 3, Appli
7	1398.2	92.3	5877	US-10-028-946-3	Sequence 3, Appli
8	1398.2	92.3	5877	US-10-791-666-3	Sequence 3, Appli
9	1398.2	92.3	6165	US-10-028-946-1	Sequence 1, Appli
10	1398.2	92.3	6165	US-10-791-666-1	Sequence 1, Appli
11	1397.8	92.3	6574	US-10-017-216-1	Sequence 1, Appli
12	1397.8	92.3	6574	US-10-325-430-10	Sequence 10, Appl

13	1397.8	92.3	6574	18	US-10-757-262-51	Sequence 51, Appl
14	1391.8	91.9	6159	13	US-10-017-216-3	Sequence 3, Appli
15	1391.8	91.9	6162	15	US-10-325-430-11	Sequence 11, Appl
16	1388	91.6	8656	18	US-10-618-941-1	Sequence 1, Appli
17	1375.8	90.8	6189	11	US-09-964-356-10	Sequence 10, Appl
18	1375.8	90.8	6189	16	US-10-262-511-1	Sequence 1, Appli
19	1375.8	90.8	6201	11	US-09-964-356-8	Sequence 8, Appli
20	1375.8	90.8	6201	16	US-10-262-511-13	Sequence 13, Appl
21	963.2	63.6	2162	15	US-10-120-988-419	Sequence 419, App
22	955.4	63.1	957	15	US-10-412-897-1	Sequence 1, Appli
23	760.8	50.2	1133	14	US-10-282-048-1	Sequence 1, Appli
24	246.8	16.3	1530	16	US-10-415-011-24	Sequence 24, Appl
25	246.8	16.3	4698	17	US-10-702-496-1	Sequence 1, Appli
26	246.8	16.3	5373	15	US-10-333-314-40	Sequence 40, Appl
27	246.8	16.3	5438	18	US-10-618-941-2	Sequence 2, Appli
28	240	15.8	6335	16	US-10-388-934-85	Sequence 85, Appl
29	238.8	15.8	5373	17	US-10-702-496-5	Sequence 5, Appli
30	236.8	15.6	4917	17	US-10-385-163-121	Sequence 121, App
31	236.8	15.6	4917	17	US-10-796-177-121	Sequence 121, App
32	234.6	15.5	2785	15	US-10-172-118-930	Sequence 930, App
33	234.6	15.5	2785	16	US-10-342-887-930	Sequence 930, App
34	234.6	15.5	5694	15	US-10-288-798-26	Sequence 26, Appl
35	234.6	15.5	5694	16	US-10-362-892-26	Sequence 26, Appl
36	234.6	15.5	7151	16	US-10-433-794-39	Sequence 39, Appl
37	231.4	15.3	2621	15	US-10-352-157-179	Sequence 179, App
38	228	15.0	5347	16	US-10-210-130-99	Sequence 99, Appl
39	228	15.0	5875	16	US-10-210-130-101	Sequence 101, App
40	225.6	14.9	3407	9	US-09-971-845-1	Sequence 1, Appli
41	225.6	14.9	3407	16	US-10-380-235-9	Sequence 9, Appli
42	216.2	14.3	174493	9	US-09-804-471A-3	Sequence 3, Appli
43	216.2	14.3	174493	14	US-10-238-709-3	Sequence 3, Appli
44	216.2	14.3	174493	16	US-10-724-594-3	Sequence 3, Appli
45	214.4	14.2	1479	9	US-09-771-161A-46	Sequence 46, Appl

## ALIGNMENTS

RESULT 1  
US-09-804-471A-1  
; Sequence 1, Application US/09804471A  
; Patent No. US20020132322A1  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01164  
; CURRENT APPLICATION NUMBER: US/09/804,471A  
; CURRENT FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-804-471A-1

Query Match	100.0%;	Score	1515;	DB	9;	Length	1515;
Best Local Similarity	100.0%;	Pred. NO.	0;				
Matches	1515;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	GGGAGATGTTGAAGTTCAAAATGAGCGCGGAATCCTTTGGATGCTGGTGTCTGAA	60				
QY	61	CCGATTCGCAACCGGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATG	120				
Db	61	CCGATTCGCAACCGGGCTCCAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTTATG	120				
QY	121	ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTTTTGTCTC	180				
Db	121	ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTTTTGTCTC	180				





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Db 1501 GCGGCTGATCCGTA 1515

RESULT 3

US-10-724-594-1  
 ; Sequence 1, Application US/10724594  
 ; Publication No. US20040091993A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001164DIV II  
 ; CURRENT APPLICATION NUMBER: US/10724,594  
 ; CURRENT FILING DATE: 2003-12-02  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1515  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-724-594-1

Query Match 100.0%; Score 1515; DB 16; Length 1515;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 CCCATGTCACACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAACCAACCTTTATG 120  
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 Db 121 ACTCAACAGCAGATGCTCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC 180  
 Qy 181 TTTGAAGAATGCAGTCAGCTGCTCTGATGAAGATTAAAGCACGTGAGCAACTTTGTCGG 240  
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 Db 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGGAAGAGACTTCGAA 300  
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 Db 301 GTCAGAACTCTGTAGGTTGTGTCACCTTTGCTGAAGTCAGGTCGTAAGAGAGAAAGCA 360  
 Qy 361 ACCGGGACATCTATGATGAAGAGTGAAGAGAGAGGCTTTATTTGGCCAGAGAGAG 420  
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1021	Db		CAAGCTTTGTTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGGTCCTTTGTCGCATCCT	1080
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1201	Db		TGCTCTCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAATCGCGTTTGTGGGG	1260
1261	QY		TTTTTCGTACAGCAAGGCACTGGGGATTCCTGGTAGATCTGATCTGTTGTGCGGCTG	1320
1261	Db		TTTTTCGTACAGCAAGGCACTGGGGATTCCTGGTAGATCTGATCTGTTGTGCGGCTG	1320
1321	QY		GACTCCCTGCCAAGACTAGCTCCATGGAAGAAAATCTTCTCATCAAAAGCAAAAGAGCTA	1380
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1381	QY		CAAGACTCTCAGGACAAGTGTCTCAAGGATTTATTTCCGACGCGGCGCTCCTTCCTGTC	1440
1381	Db		CAAGACTCTCAGGACAAGTGTCTCAAGGATTTATTTCCGACGCGGCGCTCCTTCCTGTC	1440
1441	QY		TCCAGGATCTCCCGTCCGTATATGCCAAGGGATCCGCCGGGGCGGTGCTGGCTCTGA	1500
1441	Db		TCCAGGATCTCCCGTCCGTATATGCCAAGGGATCCGCCGGGGCGGTGCTGGCTCTGA	1500
1501	QY		GCCGCTGATCCGTA	1515
1501	Db		GCCGCTGATCCGTA	1515

## RESULT 4

US-10-311-034-33

US-10-341-034-33 ; Sequence 33, Application US/10311034

US20040023242A1

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry

; APPLICANT: LAL, Preeti

APPLICANT: BANDMAN, Olga

APPLICANT: BOROWSKY, Mark L.

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: LU, Yan

; APPLICANT: GANDHI, Aameena R.

```

/ APPLICANT: TRIBOULEY, Catherine M.
/ APPLICANT: CHAMLA, Narinder K.
/ APPLICANT: YAO, Monique G.
/ APPLICANT: LU, Dyung Aina M.
/ APPLICANT: GREENWALD, Sara R.
/ APPLICANT: RAMKUMAR, Jayalaxmi
/ APPLICANT: GRIFFIN, Jennifer A.
/ APPLICANT: KEARNEY, Liam
/ APPLICANT: BURFORD, Neil
/ APPLICANT: NGUYEN, Danniell B.
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: HE, Ann
/ APPLICANT: THORNTON, Michael
/ APPLICANT: HAFALIA, April
/ APPLICANT: ARVIZU, Chandra S.
/ APPLICANT: GURURAJAN, Rajagopal
/ APPLICANT: LO, Terence P.
/ APPLICANT: KHAH, Farrah A.
/ APPLICANT: RECIPON, Shirley A.
/ APPLICANT: AZIMZAI, Yalda
/ APPLICANT: POLICKY, Jennifer L.
/ APPLICANT: DING, Li
/ APPLICANT: GREYER, Megan
/ APPLICANT: ELLIOTT, Vicki S.
/ APPLICANT: THANGAVELU, Kavitha
/ APPLICANT: BATRA, Sajeev
/ APPLICANT: ISON, Craig H.
/ TITLE OF INVENTION: HUMAN KINASES
/ FILE REFERENCE: PI-0125 PCT
/ CURRENT APPLICATION NUMBER: US/10/311,034
/ CURRENT FILING DATE: 2009-12-10
/ PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
/ 60/228,056
/ PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0-0
/ 25
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: PERL Program
/ SEQ ID NO 33
/ LENGTH: 2066
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CBI
/ US-10-311-034-33

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Query Match	99.7%	Score	1510.2	DB	16	Length	2066
Best Local Similarity	99.8%	Pred. No. 0;					
Matches	1512;	Conservative	0;	Mismatches	3;	Indels	0;
Gaps							
Qy	1	GGGAGAGTGTGAAGTTCAATATGAGCGCGGAATCCTTTGATGCTGGTCTGCTGAA	60				
Db	8	GGGAGAGTGTGAAGTTCAATATGAGCGCGGAATCCTTTGATGCTGGTCTGCTGAA	67				
Qy	61	CCCATTCGCAACCGGGGCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCCCTTTATG	120				
Db	68	CCCATTCGACGCGGGGCTCCAGGCTGAATCTGTCTTCCAGGGGAAACCCCTTTATG	127				
Qy	121	ACTCAACAGCAGATGTCCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC	180				
Db	128	ACTCAACAGCAGATGTCCTCTCTTTCCGAGAGGGATATTAGATGCCCTCTTTGTTCTC	187				
Qy	181	TTTGAAGAATGCAGTCAGCCTGCTCTGATGAGATTAAACACGTGAGCAACTTTGTCGG	240				
Db	188	TTTGAAGAATGCAGTCAGCCTGCTCTGATGAGATTAAACACGTGAGCAACTTTGTCGG	247				
Qy	241	AAGTATTCCGACACCATAGCTAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAA	300				
Db	248	AAGTATTCCGACACCATAGCTAGTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAA	307				
Qy	301	GTCAGAAGTCTTGTAGGTTGTGCTACTTTGCTGAAGTCAGGTGGTAAAGAGAGAAACA	360				



Query Match 92.7%; Score 1404.2; DB 16; Length 6298;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGGTCTCTGAA 60  
 Db 49 GGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGGTCTCTGAA 108  
 QY 61 CCATTGCCAAACGGGSCCTCCAGGCTGAATCTCTCCAGGGGAAACCCCTTTATG 120  
 Db 109 CCATTGCCAAACGGGSCCTCCAGGCTGAATCTCTCCAGGGGAAACCCCTTTATG 168  
 QY 121 ACTCAACAGCAGATGCTCTCTTTTCCGAGAAGGATATAGATGCCCTCTTTCTTC 180  
 Db 169 ACTCAACAGCAGATGCTCTCTTTTCCGAGAAGGATATAGATGCCCTCTTTCTTC 228  
 QY 181 TTTGAAGATGAGTCAGCTGCTCTCTGATGAAGATTAAGCAGTGAAGCAATTTCTCGG 240  
 Db 229 TTTGAAGATGAGTCAGCTGCTCTCTGATGAAGATTAAGCAGTGAAGCAATTTCTCGG 288  
 QY 241 AAGTATTCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAA 300  
 Db 289 AAGTATTCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTCGGCAAGGACTTCGAA 348  
 QY 301 GTCAGAGATCTGTAGGTTGGTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAACA 360  
 Db 349 GTCAGAGATCTGTAGGTTGGTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAACA 408  
 QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTGGCCCGAGAGCAG 420  
 Db 409 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTGGCCCGAGAGCAG 468  
 QY 421 GTTTCATTTTTGAGAGAGCGGAACATATTTATCTCGAAGCACAAAGCCCGTGGATCCCC 480  
 Db 469 GTTTCATTTTTGAGAGAGCGGAACATATTTATCTCGAAGCACAAAGCCCGTGGATCCCC 528  
 QY 481 CAATTACATGTCCTTTTCAGACACAAATACCTTTTATCTGTCATGATATCAGGCT 540  
 Db 529 CAATTACATGTCCTTTTCAGACACAAATACCTTTTATCTGTCATGATATCAGGCT 588  
 QY 541 GGAGGGACTCTGTCTCTTTTGAATAGATATGAGGACCACTTATAGTGAAGAACTGATA 600  
 Db 589 GGAGGGACTCTGTCTCTTTTGAATAGATATGAGGACCACTTATAGTGAAGAACTGATA 648  
 QY 601 CAGTTTACAGTACGCTGAGTGTATTTGGCTGTCACAGGTTTCATCTGATGGATACGTG 660  
 Db 649 CAGTTTACAGTACGCTGAGTGTATTTGGCTGTCACAGGTTTCATCTGATGGATACGTG 708  
 QY 661 CATCGAGACATCAAGCCTGAGAACATTTCTCGTTGACCGCAGGACACATCAAGCTGGT 720  
 Db 709 CATCGAGACATCAAGCCTGAGAACATTTCTCGTTGACCGCAGGACACATCAAGCTGGT 768  
 QY 721 GATTTGGATCTGCCCGGAAATATGATTCAAACAGATGGTGAATGCCAAACTCCGAT 780  
 Db 769 GATTTGGATCTGCCCGGAAATATGATTCAAACAGATGGTGAATGCCAAACTCCGAT 828  
 QY 781 GGGACCCAGATTAATGCTGCTCTGAGTGTGATGAACGGGATGGAAAGGC 840  
 Db 829 GGGACCCAGATTAATGCTGCTCTGAGTGTGATGAACGGGATGGAAAGGC 888  
 QY 841 ACTACGGCTGGATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 900  
 Db 889 ACTACGGCTGGATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 948  
 QY 901 GGGAGATCCCCTTCGACAGGAGAACCTCTGCCAGACCTTCAATCAATATGAATTC 960  
 Db 949 GGGAGATCCCCTTCGACAGGAGAACCTCTGCCAGACCTTCAATCAATATGAATTC 1008  
 QY 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAGCAGTACTTTCTTGAATCTGAT 1020  
 Db 1009 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAGCAGTACTTTCTTGAATCTGAT 1068

QY 1021 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080  
 Db 1069 CAAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1128  
 QY 1081 TTCTTCTCTAAAATTTGACTGGAACAACATTCGTAATCTCTCTCCCTCCCTTCGTTCCAC 1140  
 Db 1129 TTCTTCTCTAAAATTTGACTGGAACAACATTCGTAATCTCTCTCCCTCCCTTCGTTCCAC 1188  
 QY 1141 CTCAAGTCCGACCATGACACCTCCAAATTTTGTATGAACACAGAGAAGAAATTCGTGGTTC 1200  
 Db 1189 CTCAAGTCTGACGATGACACCTCCAAATTTTGTATGAACACAGAGAAGAAATTCGTGGTTC 1248  
 QY 1201 TCCTCTCCGTCAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGG 1260  
 Db 1249 TCCTCTCCGTCAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGGTTTGTGGG 1308  
 QY 1261 TTTTCTGATACAGCAAGCAGCTGGGATTTCTTGGTAGATCTGAGTCTGTTGTGGGCTCTG 1320  
 Db 1309 TTTTCTGATACAGCAAGCAGCTGGGATTTCTTGGTAGATCTGAGTCTGTTGTGGGCTCTG 1368  
 QY 1321 GATCCTCCGTCAGCTGAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 Db 1369 GATCCTCCGTCAGCTGAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTA 1428  
 QY 1381 CAAGACTCTCAGCAAGTGTCAAGGT 1409  
 Db 1429 CAAGACTCTCAGCAAGTGTCAAGAT 1457

RESULT 6  
 US-10-262-511-3  
 ; Sequence 3, Application US/10262511  
 ; Publication No. US20040038223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Peyman, John A.  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Ju, Jingfang  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Guo, Xiaojia (Sasha)  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Malyankar, Uriel M.  
 ; APPLICANT: Ort, Tatiana  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Catterton, Blina  
 ; APPLICANT: Ji, Weizhen  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Stone, David J.  
 ; APPLICANT: Pena, Carol E. A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Shimkets, Richard A.  
 ; APPLICANT: Rothenberg, Mark E.  
 ; APPLICANT: Leach, Martin D.  
 ; APPLICANT: Agee, Michele L.  
 ; APPLICANT: Berghs, Constance  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-462C  
 ; CURRENT APPLICATION NUMBER: US/10/262,511  
 ; CURRENT FILING DATE: 2003-05-28  
 ; PRIOR APPLICATION NUMBER: 60/326,483  
 ; PRIOR FILING DATE: 2001-10-02  
 ; PRIOR APPLICATION NUMBER: 60/373,815  
 ; PRIOR FILING DATE: 2002-04-19  
 ; PRIOR APPLICATION NUMBER: 60/327,917  
 ; PRIOR FILING DATE: 2001-10-09

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; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 3
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1870)
US-10-262-511-3

Query Match          92.3%; Score 1398.2; DB 16; Length 1870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAAATATGAGCGCGAATCCCTTTGGATGCTGCTGTAACCCATT 66
DB 14 ATGTTGAAGTTCAAATATGAGCGCGAATCCCTTTGGATGCTGCTGTAACCCATT 73

QY 67 GCCAACCGGCTCCAGGCTGAATCTGCTCCAGCGGAAACCCCTTTATGACTCAA 126
DB 74 GCCAGCGGCTCCAGGCTGAATCTGCTCCAGCGGAAACCCCTTTATGACTCAA 133

QY 127 CAGCAGATGCTCCTCTTCCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186
DB 134 CAGCAGATGCTCCTCTTCCCGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 193

QY 187 GAATGAGTCAGCTGCTGTGATGAAGATTAGCAGTCAGTACACTTTGTCGGAGATAT 246
DB 194 GAATGAGTCAGCTGCTGTGATGAAGATTAGCAGTCAGTACACTTTGTCGGAGATAT 253

QY 247 TCCGACACCATAGCTGATGTTACAGGAGCTCCAGCCTTCGCGAAAGGACTTTCGAAGTCAGA 306
DB 254 TCCGACACCATAGCTGATGTTACAGGAGCTCCAGCCTTCGCGAAAGGACTTTCGAAGTCAGA 313

QY 307 AGTCCTGTAGTTGTGCTCATTGCTGAAAGTCAGTGGTGAAGAGAAAGCAACCGGG 366
DB 314 AGTCCTGTAGTTGTGCTCATTGCTGAAAGTCAGTGGTGAAGAGAAAGCAACCGGG 373

QY 367 GACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGCGCCAGGAGGAGTTTCA 426
DB 374 GACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGCGCCAGGAGGAGTTTCA 433

QY 427 TTTTGTGAGGAGAGCGGCAATATTATCTCGAAGCACAAGCCGCTGGATCCGCCAATTA 486
DB 434 TTTTGTGAGGAGAGCGGCAATATTATCTCGAAGCACAAGCCGCTGGATCCGCCAATTA 493

QY 487 CAGTATGCTTTCCAGCACAATATCACCCTTATCTGTCATGGAATATCAGCTGGAGG 546
DB 494 CAGTATGCTTTCCAGCACAATATCACCCTTATCTGTCATGGAATATCAGCTGGAGG 553

QY 547 GACTTGTGTCATTTTGAATAGATATGAGGACAGTATGATGCAAAACCTTGATACAGTTT 606
DB 554 GACTTGTGTCATTTTGAATAGATATGAGGACAGTATGATGCAAAACCTTGATACAGTTT 613

QY 607 TACCTAGCTAGCTGATTTTGGCTGTTTCAAGCGTTCTCTGATGGGATACGTGATCGA 666
DB 614 TACCTAGCTAGCTGATTTTGGCTGTTTCAAGCGTTCTCTGATGGGATACGTGATCGA 673

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QY 667 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726
DB 674 GACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 733
QY 727 GGATCTGCGCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTTGGGACC 786
DB 734 GGATCTGCGCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCCGATTTGGGACC 793
QY 787 CCAGATTACATGGCTCCCTGAAGTGTGCTGATGAACGGGGATGGAAGGACACCTTAC 846
DB 794 CCAGATTACATGGCTCCCTGAAGTGTGCTGATGAACGGGGATGGAAGGACACCTTAC 853
QY 847 GGCCTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
DB 854 GGCCTGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
QY 907 TCCCTCTTCCGAGAGGAAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGG 966
DB 914 TCCCTCTTCCGAGAGGAAACCTCTGCCAGAACCTTCAATAACATTTATGAATTTCCAGCGG 973
QY 967 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1026
DB 974 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1033
QY 1027 TTGTTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCTGCTGCTGCTGCTGCT 1086
DB 1034 TTGTTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCTGCTGCTGCTGCTGCT 1093
QY 1087 TCTAAATTTGATGGAACAACATTCGTAACCTCTCTCCCTCCCTCTCGTTTCCCACTTCAAG 1146
DB 1094 TCTAAATTTGATGGAACAACATTCGTAACCTCTCTCCCTCCCTCTCGTTTCCCACTTCAAG 1153
QY 1147 TCCGAGGATGACCTCCCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1206
DB 1154 TCTGACGATGACCTCCCAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1213
QY 1207 CCGTGCACAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGCTTTTGGGGTTCG 1266
DB 1214 CCGTGCACAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGCTTTTGGGGTTCG 1273
QY 1267 TACAGCAGGACATGCGGATTTCTTGGTAGATCTGAGTCTGTTGTGCTGGTCTGACTCC 1326
DB 1274 TACAGCAGGACATGCGGATTTCTTGGTAGATCTGAGTCTGTTGTGCTGGTCTGACTCC 1333
QY 1327 CCGTGCACAGCTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGAC 1386
DB 1334 CCGTGCACAGCTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGAC 1393
QY 1387 TCTCAGGACAAAGTGTCAAGGT 1409
DB 1394 TCTCAGGACAAAGTGTCAAGAT 1416

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RESULT 7
US-10-028-946-3
; Sequence 3, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Priddle, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA

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Db 181 GAATGCTAGTCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTTGTCCGGAAGTAT 240  
 Qy 247 TCCGACACCATAGCTAGTGTACAGGACTCCAGCTTCGCAAGGACTTCGAAGTCAGA 306  
 Db 241 TCCGACACCATAGCTAGTGTACAGGACTCCAGCTTCGCAAGGACTTCGAAGTCAGA 300  
 Qy 307 AGCTTGTAGTGTGTGCTCACTTTGCTGAAGTGTGAGTGTGAAGAGAAAGCAACCGGG 366  
 Db 301 AGCTTGTAGTGTGTGCTCACTTTGCTGAAGTGTGAGTGTGAAGAGAAAGCAACCGGG 360  
 Qy 367 GACATCTATGCTATGAAGTGTGAAGAAAGAGGCTTTATGGCCCGAGAGAGGTTTCA 426  
 Db 361 GACATCTATGCTATGAAGTGTGAAGAAAGAGGCTTTATGGCCCGAGAGAGGTTTCA 420  
 Qy 427 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGTGATCCCCCAATTA 486  
 Db 421 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGTGATCCCCCAATTA 480  
 Qy 487 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTATGTAATATCAGCTCGAGGG 546  
 Db 481 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTATGTAATATCAGCTCGAGGG 540  
 Qy 547 GACTTGTGTCACTTTTGAATAGATGAGGACAGTGTAGATGAACCTGTATACAGTTT 606  
 Db 541 GACTTGTGTCACTTTTGAATAGATGAGGACAGTGTAGATGAACCTGTATACAGTTT 600  
 Qy 607 TACTAGCTAGCTGATTTTGGTGTTCACAGGGTTTCACTGTATGGGATACGTGATCGA 666  
 Db 601 TACTAGCTAGCTGATTTTGGTGTTCACAGGGTTTCACTGTATGGGATACGTGATCGA 660  
 Qy 667 GACATCAAGCTGAGACATCTCGTTGACCGCAGCAGGACACATCAAGCTGTGGAATTT 726  
 Db 661 GACATCAAGCTGAGACATCTCGTTGACCGCAGCAGGACACATCAAGCTGTGGAATTT 720  
 Qy 727 GGTATCTCCCGGAAAATGAATCAAAACAGATGGTGAATGCCAAAATCCCGATTGGAGC 786  
 Db 721 GGTATCTCCCGGAAAATGAATCAAAACAGATGGTGAATGCCAAAATCCCGATTGGAGC 780  
 Qy 787 CCAGATTACATGGCTCTGAAGTGTGACTGTGATGAACCGGGATGAAAGGACCACTAC 846  
 Db 781 CCAGATTACATGGCTCTGAAGTGTGACTGTGATGAACCGGGATGAAAGGACCACTAC 840  
 Qy 847 GGCCTGAGCTGTGACTGTGCTGAGTGGGCTGATTGCTATGAGATGATTTATGGGAGA 906  
 Db 841 GGCCTGAGCTGTGACTGTGCTGAGTGGGCTGATTGCTATGAGATGATTTATGGGAGA 900  
 Qy 907 TCCCCCTTCGAGAGGAACTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 966  
 Db 901 TCCCCCTTCGAGAGGAACTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 960  
 Qy 967 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTCTGATCTGATTTCAAGC 1026  
 Db 961 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTCTGATCTGATTTCAAGC 1020  
 Qy 1027 TTGTTGTGCGGCAGAGAAAGAGACTCAAGTTTGAAGGTCTTTGCTGCCATCTTTCTTC 1086  
 Db 1021 TTGTTGTGCGGCAGAGAAAGAGACTCAAGTTTGAAGGTCTTTGCTGCCATCTTTCTTC 1080  
 Qy 1087 TCTAAAATTCAGTGAAGCAACATTCGTAATCTCTCCCGCTTCGTTCCACCTCTCAG 1146  
 Db 1081 TCTAAAATTCAGTGAAGCAACATTCGTAATCTCTCCCGCTTCGTTCCACCTCTCAG 1140  
 Qy 1147 TCCGACGATCACACCTTCCAAATTTTGAATGACACAGAGAGAAATTCGTGGGTTTCATCCTCT 1206  
 Db 1141 TCTGACGATGACACCTTCCAAATTTTGAATGACACAGAGAGAAATTCGTGGGTTTCATCCTCT 1200  
 Qy 1207 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTCG 1266  
 Db 1201 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTCG 1260  
 Qy 1267 TACAGAAAGCACTGGGGATCTTTGGTGTAGATCTGAGTCTGTTGTGCGGTTCTGAGCTCC 1326  
 Db 1261 TACAGAAAGCACTGGGGATCTTTGGTGTAGATCTGAGTCTGTTGTGCGGTTCTGAGCTCC 1320

RESULT 9

US-10-028-946-1  
 ; Sequence 1, Application US/10028946  
 ; Publication No. US20020123622A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Xuanchuan  
 ; APPLICANT: Miranda, Maricar  
 ; APPLICANT: Fridgde, Carl Johan  
 ; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding  
 ; FILE REFERENCE: LEX-0289-USA  
 ; CURRENT APPLICATION NUMBER: US/10/028,946  
 ; CURRENT FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/258,335  
 ; PRIOR FILING DATE: 2000-12-27  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 6165  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-10-028-946-1

Query Match 92.3%; Score 1398.2; DB 13; Length 6165;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGATGCTGTGTGCTGAACCCATT 66  
 Db 1 ATGTTGAAGTTCAAAATATGGAGCGCGGAATCCTTTGATGCTGTGTGCTGAACCCATT 60  
 Qy 67 GCCAACCCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCAA 126  
 Db 61 GCCACCGCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACCAACCTTTATGACTCAA 120  
 Qy 127 CAGCAGATGTCTCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186  
 Db 121 CAGCAGATGTCTCTCTTCCGAGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180  
 Qy 187 GAATGCACTGAGCTGCTCTGATGAAGATTAAAGCAGTGAAGTGTGTCGGAAGTAT 246  
 Db 181 GAATGCACTGAGCTGCTCTGATGAAGATTAAAGCAGTGAAGTGTGTCGGAAGTAT 240  
 Qy 247 TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGGCTTCGGCAAGAGACTTCGAAAGTCAGA 306  
 Db 241 TCCGACACCATAGCTGAGTTTACAGGAGCTCCAGGCTTCGGCAAGAGACTTCGAAAGTCAGA 300  
 Qy 307 AGTCTGTAGTGTGTGCTCACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCAACCGGG 366  
 Db 301 AGTCTGTAGTGTGTGCTCACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCAACCGGG 360  
 Qy 367 GACATCTATGCTATGAAGTGTGAAGAGAGGCTTTATTTGGCCCGAGGAGAGGTTTCA 426  
 Db 361 GACATCTATGCTATGAAGTGTGAAGAGAGGCTTTATTTGGCCCGAGGAGAGGTTTCA 420  
 Qy 427 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGTGATCCCCCAATTA 486  
 Db 421 TTTTTCGAGGAAGCGGAAACATATTATCTCGAAGCACAAGCCCGTGTGATCCCCCAATTA 480  
 Qy 487 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTGTAATATCAGCTCGAGGG 546  
 Db 481 CAGTATGCTTTCAGGACAAAAATCACTTTATCTGTGTGTAATATCAGCTCGAGGG 540  
 Qy 547 GACTTGTGTCACTTTTGAATAGATGAGGACCAAGTGTAGTGAAGAAACCTGTATACAGTTT 606



[illegible]

RESULT 10

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RESULTS 10
US-10-791-666-1
; Sequence 1, Application US/10791666
; Publication No. US20040203297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946

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841 GGCTGGACTGTGACTGGTGGTCAGTGGCGGTGAATGCTCCTATGAGATGATTTATGGGAGA 900
907 TCCCTCTTCGACAGAGGAACTCTGCGAGAACCTTCAATAACATATGATTAATTTCCAGCGG 966
901 TCCCTCTTCGACAGAGGAACTCTGCGAGAACCTTCAATAACATATGATTAATTTCCAGCGG 960
967 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1026
961 TTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020
1027 TTGTTGTGGCGGACAGAGAGACTGAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1086
1021 TTGTTGTGGCGGACAGAGAGACTGAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
1087 TCTAAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1146
1081 TCTAAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1140
1147 TCCGAGATGACACCTTCAATTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTT 1206
1141 TCTGAGATGACACCTTCAATTTGATGAACAGAGAGAAATTCGTGGGTTTCATCTCTT 1200
1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCG 1266
1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCG 1260
1267 TACAGAGGCACTGGGATCTTGTAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1326
1261 TACAGAGGCACTGGGATCTTGTAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1320
1327 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCG 1386
1321 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGTTTTCG 1380
1387 TCTCAGCAAGTGTCAACAGT 1409
1381 TCTCAGCAAGTGTCAACAGT 1403

RESULT 11
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myotonic Dystrophy Type Prod
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-5701
; CURRENT APPLICATION NUMBER: US/10/017,216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-1

Query Match 92.3%; Score 1397.8; DB 13; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTTGGATGCTGGTCTGCTGAA 60
DB 13 GGGGAGATGTTGAAGTTCAAAATATGAGCGCGGAATCTTTTGGATGCTGGTCTGCTGAA 72
QY 61 CCATGTCGCAACCGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATG 120
DB 73 CCATGTCGCAACCGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATG 132
QY 121 ACTCAACAGCAGATGTCCTCTTCTTCCGAGAGGAGATATAGATGCGCTCTTTGTTCTC 180

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133 ACTCAACAGCAGATGTCCTCTCTTCCGAGAGGATATTAGATGCTCTTTGTTCTC 192
181 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACAGTGAAGAACTTTGTCGG 240
193 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACAGTGAAGAACTTTGTCGG 252
241 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCCTCCGCAAGAGCTTCGAA 300
253 AAGTATTTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCCTCCGCAAGAGCTTCGAA 312
301 GTCAGAGTCTTTGAGGTTGAGTCACTTTGCTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 360
313 GTCAGAGTCTTTGAGGTTGAGTCACTTTGCTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 372
361 ACCGGGACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 420
373 ACCGGGACATCTATGCTATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 432
421 GTTTCAATTTTGAAGGAGCGGAAATATTTCTCGAAGCACAAGCCCGTGGATCCCC 480
433 GTTTCAATTTTGAAGGAGCGGAAATATTTCTCGAAGCACAAGCCCGTGGATCCCC 492
481 CAATTACAGTATGCTTTTCAGGACAAATACCTTTATCTGGTCAATGATATCAGCT 540
493 CAATTACAGTATGCTTTTCAGGACAAATACCTTTATCTGGTCAATGATATCAGCT 552
541 GGAGGGACTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTGAAGTGAAGTGAAGTGAAGT 600
553 GGAGGGACTTGTCTGCTCACTTTTGAATAGATATGAGGACCAAGTGAAGTGAAGTGAAGTGAAGT 612
601 CAGTTTACCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
613 CAGTTTACCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 672
661 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGAGT 720
673 CATCGAGACATCAAGCTGAGAACATTTCTGTTGACCGCACAGGACATCAAGCTGAGT 732
721 GATTTTGGATCTGCGCGGAAATGAATTTCAAAAGATGTTGAATGCTGCTGCTGCTGCTGCTGCTGCT 780
733 GATTTTGGATCTGCGCGGAAATGAATTTCAAAAGATGTTGAATGCTGCTGCTGCTGCTGCTGCTGCT 792
781 GGGACCCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
793 GGGACCCAGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852
841 ACCTACGCGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
853 ACCTACGCGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
901 GGGAGATCCCCCTTCGAGAGGAACTCTGCGCAGAACCTTCCAGAACCTTCAATTAACATTAATTC 960
913 GGGAGATCCCCCTTCGAGAGGAACTCTGCGCAGAACCTTCCAGAACCTTCAATTAACATTAATTC 972
961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020
973 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1032
1021 CAAAGCTTTGTTGGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1033 CAAAGCTTTGTTGGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1092
1081 TTCTTCTCTAAATTTGACTGGAACCAATTCGTAACCTCTCTCCCTCCCTTTCGTTCCCAAC 1140
1093 TTCTTCTCTAAATTTGACTGGAACCAATTCGTAACCTCTCTCCCTCCCTTTCGTTCCCAAC 1152
1141 CTCAAGTCCGACGATGACACTCCAAATTTTGAATGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
1153 CTCAAGTCCGACGATGACACTCCAAATTTTGAATGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
1201 TCCTCTCGGTCGACGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTCGTTGTTG 1260

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Db 1213 TCCTCTCCGTCCAGTCCAGCCCTCAGGCTTCTCGGTGAAGAACTGCCCGTTTGTGGG 1272  
 QY 1261 TTTTCGTACCAAGCACTGGGATCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1320  
 Db 1273 TTTTCGTACCAAGCACTGGGATCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1332  
 QY 1321 GACTCCCTGCCAAGCACTAGCTCCATGTAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 Db 1333 GACTCCCTGCCAAGCACTAGCTCCATGTAAGAACTTCTCATCAAAAGCAAGAGCTA 1392  
 QY 1381 CAAGACTCTCAGGCAAGTGTCAAGGT 1409  
 Db 1393 CAAGACTCTCAGGCAAGTGTCAAGAT 1421

RESULT 12  
 US-10-325-430-10  
 ; Sequence 10, Application US/10325430  
 ; Publication No. US2003015325A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc  
 ; APPLICANT: Silos-Santiago, Inmaculada  
 ; APPLICANT: Rosenfeld, Julie Beth  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
 ; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
 ; TITLE OF INVENTION: 32838, 336 and 52908  
 ; FILE REFERENCE: MP101-294P1RNM  
 ; CURRENT APPLICATION NUMBER: US/10/325,430  
 ; CURRENT FILING DATE: 2002-12-19  
 ; PRIOR APPLICATION NUMBER: US 60/341,953  
 ; PRIOR FILING DATE: 2001-12-19  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-10-325-430-10

Query Match 92.3%; Score 1397.8; DB 15; Length 6574;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAATATGAGCGCGGAATCTTTGGATGCTGTGCTGCTGAA 60  
 Db 13 GGGGAGATGTTGAAGTTCAATATGAGCGCGGAATCTTTGGATGCTGTGCTGCTGAA 72  
 QY 61 CCATTGCAACCGGCTCCAGGCTGAATCTGTTCCAGGGGAAACCAACCTTTATG 120  
 Db 73 CCATTGCAACCGGCTCCAGGCTGAATCTGTTCCAGGGGAAACCAACCTTTATG 132  
 QY 121 ACTCAACAGCATCTCTCTTCCAGAGGAGATATAGATGCCCTCTTTGTTCTC 180  
 Db 133 ACTCAACAGCATCTCTCTTCCAGAGGAGATATAGATGCCCTCTTTGTTCTC 192  
 QY 181 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACGTCAGCACTTTGTCGG 240  
 Db 193 TTTGAAGATGAGTCAAGCTGCTCTGATGAAGATTAAGACGTCAGCACTTTGTCGG 252  
 QY 241 AGTATTCGACACCATAGCTGAGTACAGAGCTCCAGCTTCGGCAAGGACTTCGAA 300  
 Db 253 AGTATTCGACACCATAGCTGAGTACAGAGCTTCAGCTTCGGCAAGGACTTCGAA 312  
 QY 301 GTCAGAAGTCTGTAGGTTGTTGTTCACTTGTCTGAGTGTGTTAAGAGAGAGCA 360  
 Db 313 GTCAGAAGTCTGTAGGTTGTTGTTCACTTGTCTGAGTGTGTTAAGAGAGAGCA 372  
 QY 361 ACCGGGACATCTATGCTATGAAGATGAAGAGGCTTTATTTGGCCAGGAGAG 420  
 Db 373 ACCGGGACATCTATGCTATGAAGATGAAGAGGCTTTATTTGGCCAGGAGAG 432  
 QY 421 GTTTCATTTTGGAGAGAGCGGAACATATTTATCTCGAAGCAAGCCGCTGATCCC 480

Db 433 GTTTCATTTTTCAGGAGAGCGGAACATATTTATCTCGAAGCAAGCCCGTGGATCCCC 492  
 QY 481 CAATTACAGTATGCTTTTCAGGACAAAATACCTTTTATCTGTCATCGAATATCAGCT 540  
 Db 493 CAATTACAGTATGCTTTTCAGGACAAAATACCTTTTATCTGTCATCGAATATCAGCT 552  
 QY 541 GAGGGGACTTCTGTCATCTTTGAATAGATAGAGGACCACTAGATGAAACCTGATA 600  
 Db 553 GAGGGGACTTCTGTCATCTTTGAATAGATAGAGGACCACTAGATGAAACCTGATA 612  
 QY 601 CAGTTTACCTAGCTGAGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTG 660  
 Db 613 CAGTTTACCTAGCTGAGCTGATTTGGCTGTTTCAGAGGTTTCATCTGATGGGATACGTG 672  
 QY 661 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGTGTG 720  
 Db 673 CATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGTGTG 732  
 QY 721 GATTTGGATCTGCCCGGAAAATGAATTCAAAACAGATGTTGAATGCCAACTCCGAT 780  
 Db 733 GATTTGGATCTGCCCGGAAAATGAATTCAAAACAGATGTTGAATGCCAACTCCGAT 792  
 QY 781 GGGACCCAGATTAACATGCTCTCTGAAAGTCTGACTGTGATCAACCGGGATGAAAAGGC 840  
 Db 793 GGGACCCAGATTAACATGCTCTCTGAAAGTCTGACTGTGATCAACCGGGATGAAAAGGC 852  
 QY 841 ACTACGGCTGAGCTGAGTCTGTTGGTTCAGTGGGCTGATTTGCCATAGAGATGATTTAT 900  
 Db 853 ACTACGGCTGAGCTGAGTCTGTTGGTTCAGTGGGCTGATTTGCCATAGAGATGATTTAT 912  
 QY 901 GGGAGATCCCTCTGCGAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGAATTC 960  
 Db 913 GGGAGATCCCTCTGCGAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGAATTC 972  
 QY 961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTTGTGATCTGAT 1020  
 Db 973 CAGCGGTTTTGAAATTTCCAGATGACCCCAAGTGAGCAGTGAATTTTGTGATCTGAT 1032  
 QY 1021 CAAGCTTTGTTGTCGGCCAGAGAGAGACTGAAGTTTGAAGGTTCTTGTGCTGCCATCCT 1080  
 Db 1033 CAAGCTTTGTTGTCGGCCAGAGAGAGACTGAAGTTTGAAGGTTCTTGTGCTGCCATCCT 1092  
 QY 1081 TTCTTCTCTAAAATGACTGGAACCAATTCGTAATCTCTCTCCCTCCCTTCGTTCCACC 1140  
 Db 1093 TTCTTCTCTAAAATGACTGGAACCAATTCGTAATCTCTCTCCCTCCCTTCGTTCCACC 1152  
 QY 1141 CTCAGTCCGACGATGACACCTCCAAATTTTGAAGAACAGAGAAATTCGTTGGTTTCA 1200  
 Db 1153 CTCAGTCCGACGATGACACCTCCAAATTTTGAAGAACAGAGAAATTCGTTGGTTTCA 1212  
 QY 1201 TCCTCTCCCTGCGAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGCTTTGCGGG 1260  
 Db 1213 TCCTCTCCCTGCGAGCTGAGCCCTCAGGCTTCTCGGTTGAAGAACTGCGCTTTGCGGG 1272  
 QY 1261 TTTTCGTACAGCAAGGCACTGGGATTTTGTGATGATCTGAGTCTGTTGTGTCGGGTCTG 1320  
 Db 1273 TTTTCGTACAGCAAGGCACTGGGATTTTGTGATGATCTGAGTCTGTTGTGTCGGGTCTG 1332  
 QY 1321 GACTCCCTCCCAAGCAAGTCCATGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 Db 1333 GACTCCCTCCCAAGCAAGTCCATGAAAGAACTTCTCATCAAAAGCAAGAGCTA 1392  
 QY 1381 CAAGACTCTCAGGCAAGTGTCAAGGT 1409  
 Db 1393 CAAGACTCTCAGGCAAGTGTCAAGAT 1421

RESULT 13  
 US-10-757-262-51  
 ; Sequence 51, Application US/10757262  
 ; Publication No. US20040197825A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Karicheti, Venkateswarlu

```
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MP103-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)....(6180)
; US-10-757-262-51

Query Match      92.3%; Score 1397.8; DB 18; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1  GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGGTCTGTA 60
DB      13  GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTTGGATGCTGGTCTGTA 72

QY      61  CCCATTGCCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 120
DB      73  CCCATTGCCAGCGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 132

QY      121  ACTCAACAGCAGATGCTCTCTTTCCGAGAGGGAATATAGATGCCCTCTTTGTTCTC 180
DB      133  ACTCAACAGCAGATGCTCTCTTTCCGAGAGGGAATATAGATGCCCTCTTTGTTCTC 192

QY      181  TTTGAAGAATGCACTCAGCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCGG 240
DB      193  TTTGAAGAATGCACTCAGCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCGG 252

QY      241  AAGTATTCGACACCATAGCTAGTGTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAA 300
DB      253  AAGTATTCGACACCATAGCTAGTGTACAGGAGCTCCAGCTTCGGCAAGGACTTCGAA 312

QY      301  GTCAGAAGCTCTTAGTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGGAAGCA 360
DB      313  GTCAGAAGCTCTTAGTGTGCTCACTTTGCTGAAGTGCAGTGTGAAGAGGAAGCA 372

361  ACCGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCGAGAGCAG 420
DB      373  ACCGGGACATCTATGCTATGAAAGTGATGAAGAGAGGCTTTATTGGCCCGAGAGCAG 432

QY      421  GTTTCATTTTGGAGGAGAGCGGAAACATATTATCTGAAGCACAAGCCCGTGGATCCCC 480
DB      433  GTTTCATTTTGGAGGAGAGCGGAAACATATTATCTGAAGCACAAGCCCGTGGATCCCC 492

QY      481  CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTCATGATATCAGCCT 540
DB      493  CAATTACAGTATGCTTTTCAGGACAAAATCACCTTTATCTGGTCATGATATCAGCCT 552

QY      541  GGAGGGGACTTGTCTGTCTCACTTTTGAATAGATATAGAGCAGGAGTGTAGATGAAACCTGATA 600
DB      553  GGAGGGGACTTGTCTGTCTCACTTTTGAATAGATATAGAGCAGGAGTGTAGATGAAACCTGATA 612

QY      601  CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAAGCGTTTCACTCTGATGGGATACGTG 660
DB      613  CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAAGCGTTTCACTCTGATGGGATACGTG 672

QY      661  CATCGAGACATCAAGCCCTGAGAACATTTCTGTTTCAAGCGCAGCAGACACATCAAGCTGGTG 720
DB      673  CATCGAGACATCAAGCCCTGAGAACATTTCTGTTTCAAGCGCAGCAGACACATCAAGCTGGTG 732

QY      721  GATTTTGGATCTGCGCGGAAATGAATTCAAACAAAGATGTGAATGCCAACTCCCGATT 780
DB      733  GATTTTGGATCTGCGCGGAAATGAATTCAAACAAAGATGTGAATGCCAACTCCCGATT 792

QY      781  GGGACCCCGAGATATACATGGCTCCCTGAAGTGTGCTGACTGTGATGAACGGGGATGGAAGGC 840
DB      793  GGGACCCCGAGATATACATGGCTCCCTGAAGTGTGCTGACTGTGATGAACGGGGATGGAAGGC 852

QY      841  ACCTACGCGCTGGACTGTGACTGTGTTGTTGCTGAGTGGGCGTGTATGCTTATGAGATGATTAT 900
DB      853  ACCTACGCGCTGGACTGTGACTGTGTTGTTGCTGAGTGGGCGTGTATGCTTATGAGATGATTAT 912

QY      901  GGGAGATCCCGCTTCGCGAGAGGGAACCTCTGCCAGAACCTCTGCCAGAACCTTCAATACATTTGAATTC 960
DB      913  GGGAGATCCCGCTTCGCGAGAGGGAACCTCTGCCAGAACCTTCAATACATTTGAATTC 972

QY      961  CAGCGGTTTTTGAATAATTTCCAGATGACCCCAAGTGTGAGTGTGCTGCTGCTGCTGCTGCT 1020
DB      973  CAGCGGTTTTTGAATAATTTCCAGATGACCCCAAGTGTGAGTGTGCTGCTGCTGCTGCTGCT 1032

QY      1021  CAAAGCTTTGTTGCGCGCGGAGAGAGAGACTGAAAGTTTGAAGTGTGCTGCTGCTGCTGCT 1080
DB      1033  CAAAGCTTTGTTGCGCGCGGAGAGAGAGACTGAAAGTTTGAAGTGTGCTGCTGCTGCTGCT 1092

QY      1081  TTCTTCTCTAAATTTGACTGGAAACAACATTCGTAACCTCTCTCCCGCTTCTGTTCCACCC 1140
DB      1093  TTCTTCTCTAAATTTGACTGGAAACAACATTCGTAACCTCTCTCCCGCTTCTGTTCCACCC 1152

QY      1141  CTCAGTCCGACGATGACCTCCAAATTTTGAAGACGAGAGAGAAATTCGTGGGTTTCA 1200
DB      1153  CTCAGTCCGACGATGACCTCCAAATTTTGAAGACGAGAGAGAAATTCGTGGGTTTCA 1212

QY      1201  TCCTCTCGTCCGACGATGACCTCCAGGCTTCTCGGTTGAGAGTGTGCTGCTGCTGCTGCTG 1260
DB      1213  TCCTCTCGTCCGACGATGACCTCCAGGCTTCTCGGTTGAGAGTGTGCTGCTGCTGCTGCTG 1272

QY      1261  TTTTCGTACAGCAAGGACCTGGGGATCTTGGTGTAGATCTGAGTCTGTGTGTGCTGGGCTG 1320
DB      1273  TTTTCGTACAGCAAGGACCTGGGGATCTTGGTGTAGATCTGAGTCTGTGTGTGCTGGGCTG 1332

QY      1321  GACTCCCGCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAGCAAGAGAGCTA 1380
DB      1333  GACTCCCGCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCATCAAGCAAGAGAGCTA 1392

QY      1381  CAAGACTCTCAGGACAAAGTGTCAAGGT 1409
DB      1393  CAAGACTCTCAGGACAAAGTGTCAAGAT 1421
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RESULT 14  
US-10-017-216-3  
; Sequence 3, Application US/10017216  
; Publication No. US20020160493A1  
; GENERAL INFORMATION:  
; APPLICANT: KAPPELLE, LIBERMAN, Rosana  
; TITLE OF INVENTION: 13245, A No. US20020160493A1 Human Myotonic Dystrophy Type Prob  
; FILE OF INVENTION: Kinase and Uses Therefor  
; FILE REFERENCE: 10147-57U1  
; CURRENT APPLICATION NUMBER: US/10/017,216  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/242,429  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 6159  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-017-216-3

Query Match 91.9%; Score 1391.8; DB 13; Length 6159;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY	7	ATGTTGAAGTTCAATATGAGCGGGGAAATCCTTTGGATGCTGGTGGCTGAACCCATTT	66
DB	1	ATGTTGAAGTTCAATATGAGCGGGGAAATCCTTTGGATGCTGGTGGCTGAACCCATTT	60
QY	67	GCCAAACCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAA	126
DB	61	GCCAGCGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACACCCCTTTATGACTCAA	120
QY	127	CAGCAGATGCTCCTTTTCCGAGAGGATATAGATGCTCTTTGTTCTCTTTGAA	186
DB	121	CAGCAGATGCTCCTTTTCCGAGAGGATATAGATGCTCTTTGTTCTCTTTGAA	180
QY	187	GAATCAGTCAGCTGCTCTGATGAAGATTAAGCAGCTGAGCACTTTGTCGGAAGTAT	246
DB	181	GAATCAGTCAGCTGCTCTGATGAAGATTAAGCAGCTGAGCACTTTGTCGGAAGTAT	240
QY	247	TCCGACACCATAGCTGAGTTACAGGAGTCCAGCCCTTCGCAAGAGCTTCCAAAGTCAGA	306
DB	241	TCCGACACCATAGCTGAGTTACAGGAGTCCAGCCCTTCGCAAGAGCTTCCAAAGTCAGA	300
QY	307	AGTCTGTAGTGTGTTGCTCACTTTCTGAGTGCAGGTGTTAAGAGAGAAAGCAACCGG	366
DB	301	AGTCTGTAGTGTGTTGCTCACTTTCTGAGTGCAGGTGTTAAGAGAGAAAGCAACCGG	360
QY	367	GACATCTATGCTATGAAAGTATGAAGAGAGGCTTTATTTGGCCCGAGGAGCAGTTTCA	426
DB	361	GACATCTATGCTATGAAAGTATGAAGAGAGGCTTTATTTGGCCCGAGGAGCAGTTTCA	420
QY	427	TTTTTTGAGAGAGCGGAACTATATCTGAAACACAGCCCTGTGATCCCAATTA	486
DB	421	TTTTTTGAGAGAGCGGAACTATATCTGAAACACAGCCCTGTGATCCCAATTA	480
QY	487	CAGTATGCTTTTCCAGACAAAATCACCTTTATCTGTTGATGGAATATCAGCTGGAGG	546
DB	481	CAGTATGCTTTTCCAGACAAAATCACCTTTATCTGTTGATGGAATATCAGCTGGAGG	540
QY	547	GACTTGCTCTCATTTTGAATAGATATGAGGACCAAGTTAGTAAACCTGATCAGTTT	606
DB	541	GACTTGCTCTCATTTTGAATAGATATGAGGACCAAGTTAGTAAACCTGATCAGTTT	600
QY	607	TACCTAGCTGAGCTGATTTTGGCTGTTTACACGCTTCTGATGGGATAGTGCATCGA	666
DB	601	TACCTAGCTGAGCTGATTTTGGCTGTTTACACGCTTCTGATGGGATAGTGCATCGA	660
QY	667	GACATCAAGCCTGAGAACTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTT	726
DB	661	GACATCAAGCCTGAGAACTTCTGTTGACCGCAGGACACATCAAGCTGGTGGATTTT	720

QY	727	GGATCTGCGCGGAAATGAATTCAAAAGATGGTGAATGCCAAATCCCGATTGGGACC	786
DB	721	GGATCTGCGCGGAAATGAATTCAAAAGATGGTGAATGCCAAATCCCGATTGGGACC	780
QY	787	CCAGATTACATGCTCTCTGAGTCTGACTGTGATGAACGGGGATGAAAAGCACCTTAC	846
DB	781	CCAGATTACATGCTCTCTGAGTCTGACTGTGATGAACGGGGATGAAAAGCACCTTAC	840
QY	847	GGCTTGACATGCTGACTGGTGGTCAAGTGGCGTGAATTCCTATGAGATGATTTATGGAGA	906
DB	841	GGCTTGACATGCTGACTGGTGGTCAAGTGGCGTGAATTCCTATGAGATGATTTATGGAGA	900
QY	907	TCCCTCTTCGACAGGAGAACCTCTGCGAGAACCTTCAATAACATTAATGATTTTCCAGCGG	966
DB	901	TCCCTCTTCGACAGGAGAACCTCTGCGAGAACCTTCAATAACATTAATGATTTTCCAGCGG	960
QY	967	TTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTCTGATCTGATTTCAAAGC	1026
DB	961	TTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTCTTTCTTCTGATCTGATTTCAAAGC	1020
QY	1027	TTGTTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCGCATCCTTTCTTC	1086
DB	1021	TTGTTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCGCATCCTTTCTTC	1080
QY	1087	TCTAAATTAAGTACGAGAACCAATTCGTAATCTCTCCCTCCCTTGGTTCCTCCACCTCAAG	1146
DB	1081	TCTAAATTAAGTACGAGAACCAATTCGTAATCTCTCCCTCCCTTGGTTCCTCCACCTCAAG	1140
QY	1147	TCCGACGATGACACCTTCAATTTTGTATGAACACAGAGAGAAATTCGTGGTTCCTCTCT	1206
DB	1141	TCTGACGATGACACCTTCAATTTTGTATGAACACAGAGAGAAATTCGTGGTTCCTCTCT	1200
QY	1207	CCGTGCGAGTGAAGCTTCTCGGTGAGAACTGCCGTTTGTGGGTTTCG	1266
DB	1201	CCGTGCGAGTGAAGCTTCTCGGTGAGAACTGCCGTTTGTGGGTTTCG	1260
QY	1267	TACAGCAAGCACTGGGATCTTGTGTAGATCTGAGTCTGTTGTGCGGCTTGGAGCTCC	1326
DB	1261	TACAGCAAGCACTGGGATCTTGTGTAGATCTGAGTCTGTTGTGCGGCTTGGAGCTCC	1320
QY	1327	CCTGCCAAGACTAGTCTTCAATGGAAGAACTTCTCATCAAAAGCAAGAGCTACAGAC	1386
DB	1321	CCTGCCAAGACTAGTCTTCAATGGAAGAACTTCTCATCAAAAGCAAGAGCTACAGAC	1380
QY	1387	TCTCAGAGCAAGTGTCACAAGGT	1409
DB	1381	TCTCAGAGCAAGTGTCACAAGAT	1403

## RESULT 15

US-10-325-430-11  
; Sequence 11, Application US/10325430  
; Publication No. US20030153525A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Rosenfeld, Julie Beth  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING  
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,  
; FILE REFERENCE: WPI01-294PIRNM  
; CURRENT APPLICATION NUMBER: US/10/325,430  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/341,953  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 6162  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:

; NAME/KEY: CDS									
; LOCATION: (1)....(6162)									
US-10-325-430-11									
Query Match 91.98; Score 1391.8; DB 15; Length 6162;									
Best Local Similarity 99.58; Pred. No. 0;									
Matches 1396; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
Qy	7	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCCTTTTGGATGCTGGTGTGCTGCTGAACCCATT	66						
Db	1	ATGTTGAAGTTCAAAATATGAGCGCGGAATCCCTTTTGGATGCTGGTGTGCTGCTGAACCCATT	60						
Qy	67	GCCAAACCGGCTCCAGCGTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGATCAA	126						
Db	61	GCCAGCGGGCTCCAGCGTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGATCAA	120						
Qy	127	CAGCAGATGCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTGTCTCTTTGAA	186						
Db	121	CAGCAGATGCTCCTCTTCCCGAGAGGGATATTAGATGCCCTCTTGTCTCTTTGAA	180						
Qy	187	GAATGCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCCGGAAGTAT	246						
Db	181	GAATGCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGCTGAGCAACTTTGTCCGGAAGTAT	240						
Qy	247	TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGSCAAAGGACTTCGAGTCAGA	306						
Db	241	TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGSCAAAGGACTTCGAGTCAGA	300						
Qy	307	AGCTTCTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTTAAGAGAAAGCAACCGGG	366						
Db	301	AGCTTCTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTTAAGAGAAAGCAACCGGG	360						
Qy	367	GACATCTATGCTATGAAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	426						
Db	361	GACATCTATGCTATGAAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	420						
Qy	427	TTTTTTGAGGAAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTA	486						
Db	421	TTTTTTGAGGAAGCGGAAACATATTATCTCGAAGCACAGCCCGTGGATCCCCCAATTA	480						
Qy	487	CAGTATGCCCTTTTCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCTGGAGG	546						
Db	481	CAGTATGCCCTTTTCAGGACAAAATACCTTTATCTGTCATGGAATATCAGCCTGGAGG	540						
Qy	547	GACTTGTCTGCTCACTTTTGAATAGATATGAGGACAGCTAGATGAAAACCTGATACAGTTT	606						
Db	541	GACTTGTCTGCTCACTTTTGAATAGATATGAGGACAGCTAGATGAAAACCTGATACAGTTT	600						
Qy	607	TACCTAGCTGAGTGTATTTGGCTGTTTACAGCGTTTCATCTGATGGGATACGTGATCGA	666						
Db	601	TACCTAGCTGAGTGTATTTGGCTGTTTACAGCGTTTCATCTGATGGGATACGTGATCGA	660						
Qy	667	GACATCAAGCCTGAGAAACATCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	726						
Db	661	GACATCAAGCCTGAGAAACATCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT	720						
Qy	727	GGATCTCCCGGAAATGAAATCAAAACAGATGGTGAATGCCAAATCCCGATTGGGACC	786						
Db	721	GGATCTCCCGGAAATGAAATCAAAACAGATGGTGAATGCCAAATCCCGATTGGGACC	780						
Qy	787	CCAGATTACATGGCTCCTGAAGTGTGCTGATGAACCGGGATGGAAAAGGCACCTAC	846						
Db	781	CCAGATTACATGGCTCCTGAAGTGTGCTGATGAACCGGGATGGAAAAGGCACCTAC	840						
Qy	847	GGCTGAGCTGTGATGGTGTGCTGATGGGCTGATTCCTATGAGATGATTTATGGAGA	906						
Db	841	GGCTGAGCTGTGATGGTGTGCTGATGGGCTGATTCCTATGAGATGATTTATGGAGA	900						
Qy	907	TCCCCCTTCGAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG	966						
Db	901	TCCCCCTTCGAGAGGAACTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG	960						
Qy	967	TTTTTGAATTTCCAGATGAGCCCCAAAGTGAGCAGTGAATTTCTTGATCTGATTCAAAGC	1026						

Search completed: November 8, 2004, 10:40:20  
Job time : 778 secs

Db	961	TTTTTGAATTTCCAGATGAGCCCCAAAGTGAGCAGTGAATTTCTTGATCTGATTCATAAAGC	1020
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Db	1021	TTGTTGTGCGGCCGAGAGAGAGAGTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC	1080
Qy	1087	TCTAAAATTGACTGGAAACAACATTCGTAACTCTCTCCCCCTTCGTTCCACCCCTCAAG	1146
Db	1081	TCTAAAATTGACTGGAAACAACATTCGTAACTCTCTCCCCCTTCGTTCCACCCCTCAAG	1140
Qy	1147	TCCGACGATGACACCTCCAAATTTGATGAACGAGAGAGAAATTCGTGGGTTTCATCTCT	1206
Db	1141	TCTGACGATGACACCTCCAAATTTGATGAACGAGAGAGAAATTCGTGGGTTTCATCTCT	1200
Qy	1207	CGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGTTTTTCG	1266
Db	1201	CGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGTTTTTCG	1260
Qy	1267	TACAGCAAGGCACTGGGGAATTTGGTAGATCTGAGTCTGTGTGTGCGGTTCTGGACTCC	1326
Db	1261	TACAGCAAGGCACTGGGGAATTTGGTAGATCTGAGTCTGTGTGTGCGGTTCTGGACTCC	1320
Qy	1327	CCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCTCATCAAAGCAAGAGCTACAAGAC	1386
Db	1321	CCTGCCAAGACTAGCTCCATGGAAGAAACTTCTCTCATCAAAGCAAGAGCTACAAGAC	1380
Qy	1387	TCTCAGGACAAAGTGTCAAGGT	1409
Db	1381	TCTCAGGACAAAGTGTCAAGAT	1403

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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 01:59:29 ; Search time 726 Seconds  
(without alignments)  
10954.370 Million cell updates/sec

Title: US-10-724-594-1

Perfect score: 1515

Sequence: 1 gggagatgttgagttcaa.....tctgagccgcgcgcgta 1515

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseqn\_23Sep04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	100.0	1515	8 ACA61394	ACA61394 cDNA enco
2	1515	100.0	1515	10 AAD59938	Aad59938 Human kin
3	1515	100.0	1515	12 ADO40591	Ado40591 Human kin
4	1510.2	99.7	2066	6 AAD26454	Aad26454 Human kin
5	1505.8	99.4	1765	10 AB268726	Ab268726 Nucleotid
6	1481.8	97.8	1485	10 AB268725	Ab268725 Nucleotid
7	1404.2	92.7	6298	6 AAD38864	Aad38864 Human kin
8	1398.2	92.3	1870	8 ADA05643	Ada05643 Human NOV
9	1398.2	92.3	5877	6 ABQ78871	Abq78871 Human kin
10	1398.2	92.3	6156	9 AAL55217	Aal55217 Human CRI
11	1398.2	92.3	6165	6 ABQ78870	Abq78870 Human kin
12	1398.2	92.3	6165	9 AAL55214	Aal55214 Human CRI
13	1398.2	92.3	8603	6 AAL55215	Aal55215 Human CRI
14	1397.8	92.3	6574	6 AAD39191	Aad39191 Human MDP
15	1397.8	92.3	6574	10 ADF60992	Adf60992 Pain asso
16	1395	92.1	1870	12 ADM62808	Adm62808 Human NOV
17	1391.8	91.9	6162	10 ADF60993	Adf60993 ORF of pa
18	1388	91.6	8656	12 ADJ96544	Adj96544 Human cit
19	1382	91.2	6159	4 AAS06701	Aas06701 Polynucle
20	1375.8	90.8	6189	6 ABS83436	Abs83436 RRC/RAC-i
21	1375.8	90.8	6189	8 ADA05641	Ada05641 Human NOV

22	1375.8	90.8	6189	12 ADN62806	Adn62806 Human NOV
23	1375.8	90.8	6201	6 ABS63435	Abs63435 Human cDN
24	1375.8	90.8	6201	8 ADA05653	Ada05653 Human NOV
25	1375.8	90.8	6201	12 ADN62818	Adn62818 Human NOV
26	1158	76.4	2380	10 AB268776	Ab268776 Nucleotid
27	963.2	63.6	2162	8 ABX71191	Abx71191 Novel hum
28	955.4	63.1	957	11 ADN62729	Adn62729 Human cit
29	940.8	62.1	1048	5 AAS79753	Aas79753 DNA enco
30	760.8	50.2	1133	10 ADJ79946	Adj79946 Human kin
31	578.8	38.2	2896	5 ABV30132	Abv30132 Human pro
32	441.8	28.2	446	5 ABV15823	Abv15823 Human pro
33	434.4	28.7	485	5 ABV45624	Abv45624 Human pro
34	247.2	16.3	3835	8 ABT33346	Abt33346 NOX DNA
35	247.2	16.3	3985	8 ABT33347	Abt33347 NOX DNA
36	246.8	16.3	1530	6 AAD38845	Aad38845 Human kin
37	246.8	16.3	4698	12 ADP47966	Adp47966 Human MRC
38	246.8	16.3	4707	12 ADF95101	Adf95101 Human ser
39	246.8	16.3	4944	12 ADF95099	Adf95099 Human ser
40	246.8	16.3	5373	6 AAD30567	Aad30567 Human kin
41	246.8	16.3	5438	12 ADJ96545	Adj96545 Human dys
42	246.8	16.3	5619	12 ADI40903	Adi40903 Human kin
43	246.8	16.3	5973	10 ADC99116	Adc99116 Human KPP
44	238.8	15.8	5373	12 ADP47970	Adp47970 Human PKI
45	236.8	15.6	5094	12 ADK71883	Adk71883 Human kin

## ALIGNMENTS

RESULT 1  
ACA61394  
ID ACA61394 standard; cDNA; 1515 BP.  
XX  
AC ACA61394;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE cDNA encoding novel human kinase.  
XX  
KW Human; ss; gene; gene therapy; kinase; antisense.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 5'UTR 1..6 /\*tag= a  
FT CDS 7..1500 /\*tag= b  
FT FT /product= "Kinase"  
FT 3'UTR 1501..1515 /\*tag= c  
XX  
US2003022340-A1.  
PN 30-JAN-2003.  
XX  
PD 11-SEP-2002; 2002US-00238709.  
XX  
PR 13-MAR-2001; 2001US-00804471.  
XX  
PA (APPL-) APPLERA CORP.  
XX  
PI Webster M, Yan C, Di Francesco V, Beasley EM;  
XX  
DR WPI: 2003-438978/41.  
XX  
DR P-PSDB; ABU10126.  
XX  
PT New human kinase peptides useful as models or targets for the development  
XX  
PT of therapeutic agents that modulate kinase activity, for eliciting immune  
XX  
PT response, and in identifying compounds that modulate kinase activity or  
XX  
XX expression.  
PS Claim 4; Fig 1; 207pp; English.





FH Key Location/Qualifiers  
 FT 1..6  
 FT /\*tag= a  
 CDS 7..1500  
 FT /\*tag= b  
 FT /product= "Human kinase protein"  
 FT 1501..1515  
 FT /\*tag= c  
 XX  
 XX US2002132322-A1.  
 XX  
 XX  
 PD 19-SEP-2002.  
 XX  
 XX 13-MAR-2001; 2001US-00804471.  
 XX  
 XX 13-MAR-2001; 2001US-00804471.  
 XX (WEBS/) WEBSTER M.  
 PA (YANC/) YAN C.  
 PA (DPR/) DI FRANCESCO V.  
 PA (BEAS/) BEASLEY E M.  
 XX  
 PI Webster M, Yan C, Di Francesco V, Beasley EM;  
 XX  
 XX WPI: 2003-687480/65.  
 DR P-PSDB; AAE39504.  
 XX  
 XX New isolated human kinase proteins, useful as models for developing human  
 FT therapeutic targets, or for treating a disorder associated with an  
 FT absence of, inappropriate or unwanted expression of the protein, e.g.  
 FT cancer.  
 XX  
 XX Claim 4; Fig 1; Opp; English.  
 PS  
 XX  
 CC The present invention relates to human kinase proteins and nucleic acids  
 CC encoding them all of which are useful in the development of human  
 CC therapeutics and diagnostic composition and methods. The invention is  
 CC useful as models for the development of human therapeutic targets, aid in  
 CC the identification of therapeutic proteins and serve as targets for the  
 CC development of human therapeutic agents. The invention is also useful in  
 CC drug screening assays, in assays to determine the biological activity of  
 CC the protein, to raise antibodies and to elicit another immune response.  
 CC The antibodies are useful in pharmacogenomic analysis, for inhibiting  
 CC protein function and for tissue typing. The transgenic animals are useful  
 CC for studying the function of kinase protein, identifying and evaluating  
 CC modulators of kinase protein activity. The invention is also used in gene  
 CC therapy. The present sequence is the human kinase cDNA. The human kinase  
 CC gene is located on chromosome 12  
 XX  
 SQ Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1515; DB 10; Length 1515;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGAGATGTTGAAGTTCAATATGGAGCGCGAATCTTTTGGATGCTGGTGTGCTGAA 60  
 DB 1 GGGGAGATGTTGAAGTTCAATATGGAGCGCGAATCTTTTGGATGCTGGTGTGCTGAA 60  
 QY 61 CCNATGCCAACCGGGCTCAGGCTGAATCTGTCTTCAGGGGAAACACCCCTTATG 120  
 DB 61 CCCATTGCCAACCGGGCTCAGGCTGAATCTGTCTTCAGGGGAAACACCCCTTATG 120  
 QY 121 ACTCAACAGCAGATGTCTCTTTCCGAGAGGGATATTAGATGCCCTTTTGTCTC 180  
 DB 121 ACTCAACAGCAGATGTCTCTTTCCGAGAGGGATATTAGATGCCCTTTTGTCTC 180  
 QY 181 TTGAAAGATGCACTAGCTAGCTGTCTGTATGAAGATTAAAGCAGTGAACCTTTGTCGG 240  
 DB 181 TTGAAAGATGCACTAGCTAGCTGTCTGTATGAAGATTAAAGCAGTGAACCTTTGTCGG 240  
 QY 241 AAGTATTCCGACACCATAGCTAGTTACAGAGCTCCAGCTTCGGCAAGGACTTCGAA 300

DB 241 AAGTATTCCGACACCATAGCTAGTTACAGAGCTCCAGCCTTCGGCAAGGACTTCGAA 300  
 QY 301 GTCAGAGTCTTGTAGGTGTGGTCACTTTGCTGAAGTCGAGGTGGTGAAGAGAAAGCA 360  
 DB 301 GTCAGAGTCTTGTAGGTGTGGTCACTTTGCTGAAGTCGAGGTGGTGAAGAGAAAGCA 360  
 QY 361 ACCGGGGACATCTATGCTATGAAAGTGAAGAGAAAGGCTTTATTGGCCCCAGAGCAG 420  
 DB 361 ACCGGGGACATCTATGCTATGAAAGTGAAGAGAAAGGCTTTATTGGCCCCAGAGCAG 420  
 QY 421 GTTTCATTTTTCAGAGAGAGCGGAAACATATTATCTGAAGCACAAGCCCGTGGATCCCC 480  
 DB 421 GTTTCATTTTTCAGAGAGAGCGGAAACATATTATCTGAAGCACAAGCCCGTGGATCCCC 480  
 QY 481 CAATTACAGTATGCTTTTTCAGGACAAAATACCTTTTATCTGGTCAATGGAATATCAGCCT 540  
 DB 481 CAATTACAGTATGCTTTTTCAGGACAAAATACCTTTTATCTGGTCAATGGAATATCAGCCT 540  
 QY 541 GGAGGGGACTTGTCTGTCTCTTTTGAATAGATATGAGGACCAAGTTAGATGAAACCTGATA 600  
 DB 541 GGAGGGGACTTGTCTGTCTCTTTTGAATAGATATGAGGACCAAGTTAGATGAAACCTGATA 600  
 QY 601 CAGTTTTTACCTAGCTAGCTGATTTTGGCTGTTTCAACAGTGGTGAATGCCAAACTCCCGATT 660  
 DB 601 CAGTTTTTACCTAGCTAGCTGATTTTGGCTGTTTCAACAGTGGTGAATGCCAAACTCCCGATT 660  
 QY 661 CATGAGACATCAAGCCTGAGAAACATTTCTGTGACCGCACAGGACACATCAAGCTGGTG 720  
 DB 661 CATGAGACATCAAGCCTGAGAAACATTTCTGTGACCGCACAGGACACATCAAGCTGGTG 720  
 QY 721 GATTTTGGATCTGCCCGGAAATGAATTTCAACAGATGGTGAATGCCAAACTCCCGATT 780  
 DB 721 GATTTTGGATCTGCCCGGAAATGAATTTCAACAGATGGTGAATGCCAAACTCCCGATT 780  
 QY 781 GGGACCCAGATTACATGGCTCTCTGAAGTGTGATGTGATGAACGGGGATGGAAAAGGC 840  
 DB 781 GGGACCCAGATTACATGGCTCTCTGAAGTGTGATGTGATGAACGGGGATGGAAAAGGC 840  
 QY 841 ACCTAGGCTGAGCTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 900  
 DB 841 ACCTAGGCTGAGCTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 900  
 QY 901 GGGAGATCCCTTTCGAGAGAGGACCTCTGCCAGAACCTTCAATTAACATTATGAATTC 960  
 DB 901 GGGAGATCCCTTTCGAGAGAGGACCTCTGCCAGAACCTTCAATTAACATTATGAATTC 960  
 QY 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020  
 DB 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020  
 QY 1021 CAAAGCTTTGTTGGCGCCAGAAAGAGAGACTGAAGTTGAAGTTGAAGTTGAAGTTGAAGT 1080  
 DB 1021 CAAAGCTTTGTTGGCGCCAGAAAGAGAGACTGAAGTTGAAGTTGAAGTTGAAGTTGAAGT 1080  
 QY 1081 TTCTTCTCTAAATTTGACTGGAACAACTTCGTAACCTCTCTCCCTCCCTCTCTCTCCAC 1140  
 DB 1081 TTCTTCTCTAAATTTGACTGGAACAACTTCGTAACCTCTCTCCCTCCCTCTCTCTCCAC 1140  
 QY 1141 CTCAGTCCGAGCAGTACACCTCCAAATTTTGAATGAAACAGAGAGAAATTCGTTGGTTCA 1200  
 DB 1141 CTCAGTCCGAGCAGTACACCTCCAAATTTTGAATGAAACAGAGAGAAATTCGTTGGTTCA 1200  
 QY 1201 TCCTCTCGTCCAGCTGAGCCCTTCAGGCTTCTCGGTTGAAGAACTCCCGTTTGTGGGG 1260  
 DB 1201 TCCTCTCGTCCAGCTGAGCCCTTCAGGCTTCTCGGTTGAAGAACTCCCGTTTGTGGGG 1260  
 QY 1261 TTTTCGTAACAGCAGCTGGGATTTCTGGTGAATCTGGTGAATCTGGTGTGTCGGGTCG 1320  
 DB 1261 TTTTCGTAACAGCAGCTGGGATTTCTGGTGAATCTGGTGAATCTGGTGTGTCGGGTCG 1320  
 QY 1321 GACTCCCTCCAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA 1380  
 DB 1321 GACTCCCTCCAGACTAGCTCCATGGAAGAAACTTCTCATCAAAAGCAAGAGCTA 1380

QY 1381 CAAGACTCTCAGGACAAAGTGTACAAAGGTATTTATTTCCGACGGCGCTCCTTCTTGGC 1440  
 Db 1381 CAAGACTCTCAGGACAAAGTGTACAAAGGTATTTATTTCCGACGGCGCTCCTTCTTGGC 1440  
 QY 1441 TCAGGATCTCCCGTCCGCTATATGCAAGGATCCGCGCGCGCTGCTGCTCTGA 1500  
 Db 1441 TCAGGATCTCCCGTCCGCTATATGCAAGGATCCGCGCGCGCTGCTGCTCTGA 1500  
 QY 1501 GCGCCTGATCCGTA 1515  
 Db 1501 GCGCCTGATCCGTA 1515

RESULT 3  
 ADO40591  
 ID ADO40591 standard; cDNA; 1515 BP.

AC ADO40591;  
 DT 29-JUL-2004 (first entry)  
 XX Human kinase cDNA.  
 XX Kinase; rho/rae-interacting citron kinase; drug screening;  
 KW Kinase related disorder; human; chromosome 12; gene; ss.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 1..6  
 FT 5'UTR /\*tag= a  
 FT CDS 7..1500  
 FT /\*tag= b  
 FT /\*product= "Human kinase protein"  
 FT 3'UTR 1501..1515  
 FT /\*tag= c

XX US2004091993-A1.  
 XX 13-MAY-2004.  
 XX 02-DEC-2003; 2003US-00724594.  
 XX 13-MAR-2001; 2001US-00804471.  
 XX 11-SEP-2002; 2002US-00238709.  
 XX (APPL-) APPLERA CORP.  
 XX Webster M, Yan C, Di Francesco V, Beasley EM;  
 PI WPI: 2004-374957/35.  
 XX P-PSDB; ADO40592.

XX New isolated human kinase proteins and nucleic acids, useful for  
 PT developing human therapeutic targets, identifying therapeutic proteins or  
 PT serve as targets for the development of human therapeutic agents that  
 PT modulate kinase activity.

XX Claim 4; SEQ ID NO 1; 207pp; English.

XX The present invention provides a kinase polypeptide and its encoding  
 CC polynucleotide. The polypeptide and polynucleotide of the invention are  
 CC useful as models for the development of human therapeutic targets, aid in  
 CC the identification of therapeutic proteins and serve as targets for the  
 CC development of human therapeutic agents that modulate kinase activity in  
 CC cells and tissues that express the kinase. The invention is also useful  
 CC for biological assays related to kinases, in drug screening assays, for  
 CC treating disorders characterized by an absence of inappropriate and  
 CC unwanted expression of the protein. The present sequence is human kinase  
 CC cDNA. The human kinase gene is located on chromosome 12.

XX Sequence 1515 BP; 378 A; 362 C; 383 G; 392 T; 0 U; 0 Other;

Query Match  
 Best Local Similarity 100.0%; Score 1515; DB 12; Length 1515;  
 Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAGATGTTGAAGTTCAAATATGGAGCGCGAAATCCCTTTGGATGCTGTGCTGTGAA 60  
 Db 1 GGGAGATGTTGAAGTTCAAATATGGAGCGCGAAATCCCTTTGGATGCTGTGCTGTGAA 60  
 QY 61 CCCATTCCCAACCGGGCTCCAGGCTGAATCTCTTCTCCAGGGGAAACACACCTTTATG 120  
 Db 61 CCCATTCCCAACCGGGCTCCAGGCTGAATCTCTTCTCCAGGGGAAACACACCTTTATG 120  
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 QY 181 TTTGAAGATGTCAGTCCAGCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCGG 240  
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 QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCCAAGGAGCAG 420  
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 QY 421 GTTTATTTTTCAGGAAGCGGAAACATATTATCTCGAAGACAAAGCCGCTGGATCCCC 480  
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 QY 481 CAATTACAGTATGCTTTTCAGGACAAAAATCACTTTATCTGCTCATGGAATATCAGCCT 540  
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 Db 601 CAGTTTACCTAGCTAGCTGATTTTGGCTGTTTCAGAGGTTTCATCTGTGGATACGCTG 660  
 QY 661 CATCGAGACATCAAGCTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720  
 Db 661 CATCGAGACATCAAGCTGAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTG 720  
 QY 721 GATTTGGATCTCGCGGAAAATGAATTCAAACAGATGTTGATGAAATCCAACTCCGATT 780  
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 Db 781 GGGACCCAGATTACATGGCTCTCTGAAAGTCTGACCTGATGAACCGGGATGGAAGGC 840  
 QY 841 ACCTACGGCTGAGCTGTGATGCTGGTGTGATGGGGCTGATTCCTATGAGATGATTTAT 900  
 Db 841 ACCTACGGCTGAGCTGTGATGCTGGTGTGATGGGGCTGATTCCTATGAGATGATTTAT 900  
 QY 901 GGGAGATCCCTTTCCGACAGGGAACCTCTGCGAGAACCTTCAATTAACATTATGAATTC 960  
 Db 901 GGGAGATCCCTTTCCGACAGGGAACCTCTGCGAGAACCTTCAATTAACATTATGAATTC 960  
 QY 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTAGAGGAGTGAATCTTCTGATCTGATT 1020  
 Db 961 CAGCGGTTTTTGAATTTCCAGATGACCCCAAGTAGAGGAGTGAATCTTCTGATCTGATT 1020

Qy	1021	CAAAAGCTTGTTGTCGGCCGCAAGAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCCT	1081
Db	1021	CAAAAGCTTGTTGTCGGCCGCAAGAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCCT	1080
Qy	1081	TTCTTCTCTAAAATTGACTGTGAAACAAATTCGTAACTCTCTCTCCCCCTTCGTTCGCCACC	1140
Db	1081	TTCTTCTCTAAAATTGACTGTGAAACAAATTCGTAACTCTCTCTCCCCCTTCGTTCGCCACC	1140
Qy	1141	CTCAAGTCCGACGATGACACCTCCCAATTTTGATGAACACAGAGAAGAAATTCGTGGGTTTCA	1200
Db	1141	CTCAAGTCCGACGATGACACCTCCCAATTTTGATGAACACAGAGAAGAAATTCGTGGGTTTCA	1200
Qy	1201	TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCTCGGAGTGAAGAACTGCCGTTTGTGGGG	1260
Db	1201	TCCTCTCCGTGCCAGCTGAGCCCTCAGGCTTCTCGGAGTGAAGAACTGCCGTTTGTGGGG	1260
Qy	1261	TTTTTCGTACAGCAAGGCACCTGGGATTCCTTGGTAGATCTGAGTCTGTGTGCGGGTCTG	1320
Db	1261	TTTTTCGTACAGCAAGGCACCTGGGATTCCTTGGTAGATCTGAGTCTGTGTGCGGGTCTG	1320
Qy	1321	GACTCCCTCTGCCAAGCTAGCTCCATCGGAAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA	1380
Db	1321	GACTCCCTCTGCCAAGCTAGCTCCATCGGAAAGAAAGAACTTCTCATCAAAAGCAAGAGCTA	1380
Qy	1381	CAAGACTCTCAGGACAAAGTGTCAACAAAGTATTATTTCCGACGCGCGCTTCCCTTGC	1440
Db	1381	CAAGACTCTCAGGACAAAGTGTCAACAAAGTATTATTTCCGACGCGCGCTTCCCTTGC	1440
Qy	1441	TCGAGGATCTCTCCGTCGGTATATGCAAGGATTCGCGCGCGCGCTGCTGTGCTCTGA	1500
Db	1441	TCCAGGATCTCTCCGTCGGTATATGCAAGGATTCGCGCGCGCGCTGCTGTGCTCTGA	1500
Qy	1501	GCGCCCTGATCCGTA 1515	
Db	1501	GCGCCCTGATCCGTA 1515	
RESULT 4			
AAD26454			
ID	AAD26454 standard; cDNA; 2066 BP.		
XX			
AC	AAD26454;		
XX			
DT	26-MAR-2002 (first entry)		
XX			
DE	Human kinase PKIN-7 cDNA.		
XX			
KW	Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;		
KW	immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;		
KW	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;		
KW	allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;		
KW	autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;		
KW	Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;		
KW	rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;		
KW	hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;		
KW	cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;		
KW	congestive heart failure; ischaemic heart disease; lung tumour; gout;		
KW	fatty liver; Niemann-Pick's disease; gene therapy; ss.		
XX			
OS	Homo sapiens.		
XX			
PH	Key		
FT	Location/Qualifiers		
FT	14..1507		
FT	/*tag= a		
XX			
XX	/product= "Human PKIN-7 protein"		
XX			
PN	WO200196547-A2.		
XX			
XX			
PD	20-DEC-2001.		
XX			
XX	14-JUN-2001; 2001WO-US019444.		
XX			
XX	15-JUN-2000; 2000US-0212073P.		
XX			

PR	23-JUN-2000; 2000US-0213467P.
PR	30-JUN-2000; 2000US-0215651P.
PR	07-JUL-2000; 2000US-0216059P.
PR	13-JUL-2000; 2000US-0218372P.
PR	25-AUG-2000; 2000US-0228056P.
XX	(INCY-) INCYTE GENOMICS INC.
PA	
XX	
PI	Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
PI	Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
PI	Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
PI	Baughan MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI	Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX	
DR	WPI; 2002-090207/12.
DR	P-PSDB; AAE16261.
XX	
PT	New polypeptides, useful for diagnosing, treating or preventing disorders
PT	of growth and development, cardiovascular and lipid, and diseases such as
PT	cancer, comprise human kinase polypeptides.
XX	
CC	Claim 5; Page 180-181; 197pp; English.
XX	
CC	The invention relates to human kinase PKIN proteins and their
CC	corresponding cDNAs. A composition containing PKIN acnolist is useful for
CC	treating a disease or condition associated with decreased expression of
CC	PKIN and a composition comprising PKIN antagonist is useful for treating
CC	a disease or condition associated with overexpression of PKIN. The
CC	disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC	(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC	mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC	rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC	bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC	Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC	vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC	aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC	ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC	hypercholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC	of a test compound and in gene therapy. The present sequence is human
CC	PKIN-7 CDNA
XX	
SQ	Sequence 2066 BP; 515 A; 497 C; 516 G; 538 T; 0 U; 0 Other;
	Query Match 99.7%; Score 1510.2; DB 6; Length 2066;
	Best Local Similarity 99.8%; Pred. No. 0;
	Matches 1512; Conservative 0; Mismatches 3; Indels 0; Gaps 0
Qy	1 GGGGAGATGTGAATTCAATAATGGACGGCGGAATCTTTGGATGCTGGTCTCTCAA 60
Dd	8 GGGGAGATGTGAATTCAATAATGGACGGCGGAATCTTTGGATGCTGGTCTCTCAA 67
Qy	61 CCCATTGCCAACCGGGCCTTCAGGCCTGAATCTGTTTCTCCAGGGGAACCACCCCTTTATG 120
Dd	68 CCCATTGCCAGCGGGCCTCCAGGCTGAATCTGTTTCTCCAGGGGAACCACCCCTTTATG 127
Qy	121 ACTCAACAGCAGATGTCCTCTTTTCCGAGAAGGATATTAGATGCCCTCTTTGTTCTC 180
Dd	128 ACTCAACAGCAGATGTCCTCTTTTCCGAGAAGGATATTAGATGCCCTCTTTGTTCTC 187
Qy	181 TTTCAGAAATGCAGTCAGCCTGCCTCTCATGAAGATTAAACACGCTGAGCAACTTTGTCGGG 240
Dd	188 TTTCAGAAATGCAGTCAGCCTGCCTCTCATGAAGATTAAACACGCTGAGCAACTTTGTCGGG 247
Qy	241 AAGTATTCCGACACCAATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGAGCTTCGAA 300
Dd	248 AAGTATTCCGACACCAATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGAGCTTCGAA 307

QY 301 GTGAGAGTCTTGTAGTGTGCTCACTTTGCTGTAAGTGCAGGTGCTAAGAGAGAAAGCA 360  
 Db 308 GTGAGAAGTCTTGTAGTGTGCTCACTTTGCTGTAAGTGCAGGTGCTAAGAGAGAAAGCA 367  
 QY 361 ACCGGGACATCTATGCTATGAAGTGTGAAGAGAGAGGCTTTATGCGCCACGAGAGCAG 420  
 Db 368 ACCGGGACATCTATGCTATGAAGTGTGAAGAGAGAGGCTTTATGCGCCACGAGAGCAG 427  
 QY 421 GTTTTCATTTTTCAGGAGAGCGGAACATATATCTCGAAGCAGAGCCGCTGGATCCCC 480  
 Db 428 GTTTTCATTTTTCAGGAGAGCGGAACATATATCTCGAAGCAGAGCCGCTGGATCCCC 487  
 QY 481 CAATTACAGTATGCTTTTCAGGACAAAATACCTTTTATCTGGTATGAATATCAGCCT 540  
 Db 488 CAATTACAGTATGCTTTTCAGGACAAAATACCTTTTATCTGGTATGAATATCAGCCT 547  
 QY 541 GGAGGGGACTTGTGTCACATTTTGAATAGATATGAGACCAAGTATGAAACCTGATA 600  
 Db 548 GGAGGGGACTTGTGTCACATTTTGAATAGATATGAGACCAAGTATGAAACCTGATA 607  
 QY 601 CAGTTTACCTAGTGTGCTGATTTTGGCTGTTTACAGAGGTTTCATCTGATGGATACGTG 660  
 Db 608 CAGTTTACCTAGTGTGCTGATTTTGGCTGTTTACAGAGGTTTCATCTGATGGATACGTG 667  
 QY 661 CATCGAGACATCAAGCTGAGAACATCTCTGTTGACCGACAGGACACATCAAGCTGTG 720  
 Db 668 CATCGAGACATCAAGCTGAGAACATCTCTGTTGACCGACAGGACACATCAAGCTGTG 727  
 QY 721 GATTTTGGATCTCCCGAAGAAATGAAATCAAAAGATGGTGAATGCCAAATCCCGATT 780  
 Db 728 GATTTTGGATCTCCCGAAGAAATGAAATCAAAAGATGGTGAATGCCAAATCCCGATT 787  
 QY 781 GGGACCCAGATACATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 Db 788 GGGACCCAGATACATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847  
 QY 841 ACCTACGGCTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 Db 848 ACCTACGGCTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907  
 QY 901 GGGAGATCCCTTCGAGAGGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 Db 908 GGGAGATCCCTTCGAGAGGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967  
 QY 961 CAGCGGTTTTGAAATTTTCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020  
 Db 968 CAGCGGTTTTGAAATTTTCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1027  
 QY 1021 CAAAGCTTGTGTCGCGCCAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080  
 Db 1028 CAAAGCTTGTGTCGCGCCAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1087  
 QY 1081 TTCTTCTTAAATGACTGGAAACAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 Db 1088 TTCTTCTTAAATGACTGGAAACAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1147  
 QY 1141 CTCAGTTCGACGATGACACCTCCAAATTTGATGACACGAGAGAGAGTTCGTTGGTTTCA 1200  
 Db 1148 CTCAGTTCGACGATGACACCTCCAAATTTGATGACACGAGAGAGAGTTCGTTGGTTTCA 1207  
 QY 1201 TCCTCTCCGTCGAGTGCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGG 1260  
 Db 1208 TCCTCTCCGTCGAGTGCCTCAGGCTTCTCGGGTGAAGAACTGCGCTTTGTGGG 1267  
 QY 1261 TTTTCGTACAGGAGGACTGGGATCTTGTGATCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 Db 1268 TTTTCGTACAGGAGGACTGGGATCTTGTGATCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1327  
 QY 1321 GACTCCCTGCCAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTA 1380  
 Db 1328 GACTCCCTGCCAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTA 1387

QY 1381 CAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGACGCGGCTCTCTCTTC 1440  
 Db 1388 CAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGACGCGGCTCTCTCTTC 1447  
 QY 1441 TCCAGGATCTCTCCGTCGCTATATGTCACAGGATTCGCGCGGCGCTCTCTCTCTCTGA 1500  
 Db 1448 TCCAGGATCTCTCCGTCGCTATATGTCACAGGATTCGCGCGGCGCTCTCTCTCTCTGA 1507  
 QY 1501 GCCGCTGATCCGTA 1515  
 Db 1508 GCCGCTGATCCGTA 1522

RESULT 5  
 ID AB268726 standard; DNA; 1765 BP.  
 AC AB268726;  
 XX  
 DT 16-MAY-2003 (first entry)  
 XX  
 DE Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.  
 KW Human; citron rho/rac-interacting kinase-short kinase; obesity;  
 KW chronic obstructive pulmonary disease; hypertension; diabetes;  
 KW coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;  
 KW gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;  
 KW polycystic ovarian syndrome; fertility; depression; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1494  
 FT /\*tag= a  
 FT /product= "citron rho/rac-interacting kinase-short  
 FT kinase."  
 XX  
 FN WO2003004629-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 01-JUL-2002; 2002WO-EP007229.  
 XX  
 PR 02-JUL-2001; 2001US-0301853P.  
 PR 10-DEC-2001; 2001US-0337130P.  
 PR 25-APR-2002; 2002US-0375015P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Zhu Z;  
 XX  
 DR WPI; 2003-221595/21.  
 DR P-PSDB; ABP97687.  
 XX  
 CC New human citron rho/rac-interacting kinase-short kinase polypeptide and  
 CC polynucleotide for preventing or treating diseases associated with the  
 CC polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
 CC disease.  
 XX  
 PS Claim 1; Fig 18; 145pp; English.  
 CC  
 CC The present sequence encodes a human citron rho/rac-interacting kinase-  
 CC short kinase polypeptide. The polynucleotide and polypeptide of the  
 CC invention are useful in preventing, ameliorating, or treating diseases  
 CC associated with the polypeptide dysfunction. The expression vector or the  
 CC reagent is useful in the preparation of a medicament for modulating the  
 CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
 CC disease, such as obesity or chronic obstructive pulmonary disease. These  
 CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
 CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
 CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
 CC fertility, and depression

Accession	Species	Protein Name	Location/Qualifiers
1027	Db	TTTTTGAATTTTCAGATGACCCCAAGATGAGCAGTCACTTTCTTGATCTGATTCACAAGC	1027
1027	Qy	TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTCTCTGCCATCTTTCTTC	1086
1021	Db	TTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCACTCTTTCTTC	1080
1087	Qy	TCTAAAATTCAGCTGGAACAACATTCGTAACCTCTCCTCCCCCTTCGTTCCACCCCTCAAG	1146
1081	Db	TCTAAAATTCAGCTGGAACAACATTCGTAACCTCTCCTCCCCCTTCGTTCCACCCCTCAAG	1140
1147	Qy	TCCGACGATGACACCTCTCAATTTTGTATGAACACAGAGAAGAAATTCGTGGGTTTCATCTCT	1206
1141	Db	TCTGACGATGACACCTCTCAATTTTGTATGAACACAGAGAAGAAATTCGTGGGTTTCATCTCT	1200
1207	Qy	CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTTCG	1266
1201	Db	CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGGTTTGTGGGGTTTTTCG	1260
1267	Qy	TACAGCAAGGCACCTGGGATTCCTTGGTAGATCTCAGTCTGTGTGTCGGGTCTGGACTCC	1322
1261	Db	TACAGCAAGGCACCTGGGATTCCTTGGTAGATCTCAGTCTGTGTGTCGGGTCTGGACTCC	1322
1327	Qy	CCTGCCAAGCTAGCTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTCAAGAC	1388
1321	Db	CCTGCCAAGCTAGCTCCATGGAAGAAAGAACTTCTCATCAAAAGCAAGAGCTCAAGAC	1388
1387	Qy	TCTCAGACCAAGTCTCAAGAGTATTTATTTCCGACGCGGCCCTCTTCTTGTCTCCAGG	1446
1381	Db	TCTCAGACCAAGTCTCAAGAGTATTTATTTCCGACGCGGCCCTCTTCTTGTCTCCAGG	1440
1447	Qy	ATCTCCCGTCCGATATATGCAAGGATTCGCGCGGCGCGCTCTGTGCTCTGAGCCGCC	1506
1441	Db	ATCTCCCGTCCGATATATGCAAGGATTCGCGCGGCGCGCTCTGTGCTCTGAGCCGCC	1500
1507	Qy	TGATCCCGTA 1515	
1501	Db	TGATCCCGTA 1509	
RESULT 6			
ABZ68725	ID	ABZ68725 standard; DNA; 1485 BP.	
XX	AC	ABZ68725;	
XX	DT	16-MAY-2003 (first entry)	
XX	DE	Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.	
XX	KW	Human; citron rho/rac-interacting kinase-short kinase; obesity;	
XX	KW	chronic obstructive pulmonary disease; hypertension; diabetes;	
XX	KW	coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;	
XX	KW	gout; osteoarthritis; sleep apnea; cancer; thrombotic disease;	
XX	KW	polycystic ovarian syndrome; fertility; depression; gene; ss.	
OS	XX	Homo sapiens.	
XX	Key	Location/Qualifiers	
XX	FT	1..1485	
XX	FT	/*tag= a	
XX	FT	/partial	
XX	FT	/product= "citron rho/rac-interacting kinase-short	
XX	FT	kinase"	
XX	PN	WO2003004629-A2.	
XX	PD	16-JAN-2003.	
XX	PF	01-JUL-2002; 2002WO-EP007229.	
XX	PR	02-JUL-2001; 2001US-0301853P.	
XX	PR	10-DEC-2001; 2001US-0337130P.	
XX	PR	25-APR-2002; 2002US-0375015P.	

XX (FARB ) BAYER AG.  
 XX 2hu Z;  
 XX WPI; 2003-221595/21.  
 DR P-PSDB; ABP97681.  
 XX  
 XX New human citron rho/rac-interacting kinase-short kinase polypeptide and  
 PT polynucleotide for preventing or treating diseases associated with the  
 PT polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary  
 PT disease.  
 XX  
 XX Claim 1; Fig 1; 145pp; English.  
 XX  
 CC The present sequence encodes a human citron rho/rac-interacting kinase-  
 CC short kinase polypeptide. The polynucleotide and polypeptide of the  
 CC invention are useful in preventing, ameliorating, or treating diseases  
 CC associated with the polypeptide dysfunction. The expression vector or the  
 CC reagent is useful in the preparation of a medicament for modulating the  
 CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
 CC disease, such as obesity or chronic obstructive pulmonary disease. These  
 CC may also be used for treating obesity/ overweight-associated  
 CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
 CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
 CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
 CC fertility, and depression  
 XX  
 XX Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;  
 SQ  
 Query Match 97.8%; Score 1481.8; DB 10; Length 1485;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1483; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 7 ATGTTGAAGTCAAAATATGAGCGCGCGGAATCTTTGGATGCTGGTCTCAACCCCAT 66  
 1 ATGTTGAAGTCAAAATATGAGCGCGCGGAATCTTTGGATGCTGGTCTCAACCCCAT 60  
 67 GCCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCCTTTATGACTCAA 126  
 61 GCCAGCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCCTTTATGACTCAA 120  
 127 CAGCAGATGTCCTCTTTCCGAGAGGGAATATAGATGCCCTCTTTGTTCTTTGAA 186  
 121 CAGCAGATGTCCTCTTTCCGAGAGGGAATATAGATGCCCTCTTTGTTCTTTGAA 180  
 187 GAATGAGTCAAGTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCGGGAAGTAT 246  
 181 GAATGAGTCAAGTCTGATGAAGATTAAGCAGCTGAGCAACTTTGTCGGGAAGTAT 240  
 247 TCCGACACATGAGTCAAGGAGTCCAGCTTCGCGGAAAGAGCTTGAAGTCA 306  
 241 TCCGACACATGAGTCAAGGAGTCCAGCTTCGCGGAAAGAGCTTGAAGTCA 300  
 307 AGTCTTTGAGTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAACCAACCGG 366  
 301 AGTCTTTGAGTGTGCTCACTTTGCTGAAGTGCAGGTGTAAGAGAGAAACCAACCGG 360  
 367 GACATCTATGCTATGAAGTATGAAGAGAGAGGTATTTATGCGCCAGAGCAGTTTCA 426  
 361 GACATCTATGCTATGAAGTATGAAGAGAGAGGTATTTATGCGCCAGAGCAGTTTCA 420  
 427 TTTTGTGAGAGAGCGGACATATTTCTCGAAGCAGAGCCGCTGGATCCCCAATTA 486  
 421 TTTTGTGAGAGAGCGGACATATTTCTCGAAGCAGAGCCGCTGGATCCCCAATTA 480  
 487 CAGTATGCTTTTTCAGGACAAAATCACTTTATCTGTCATGGAATATCAGCTGGAGGG 546  
 481 CAGTATGCTTTTTCAGGACAAAATCACTTTATCTGTCATGGAATATCAGCTGGAGGG 540  
 547 GACTTCTGCTCACTTTTGAATAGATATGAGGACCACTTAGATGAAACCTGATACAGTTT 606  
 541 GACTTCTGCTCACTTTTGAATAGATATGAGGACCACTTAGATGAAACCTGATACAGTTT 600

QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATGATGATCGA 666  
 DB 601 TACCTAGCTGAGCTGATTTTGGCTGTTTCACAGCGTTTCATCTGATGGATGATGATCGA 660  
 QY 667 GACATCAAGCTGAGAACTTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726  
 DB 661 GACATCAAGCTGAGAACTTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720  
 QY 727 GGATCTCCGCGAAAATGAATTCAAACAGATGCTGAATGCCAAACTCCCGATGGAGACC 786  
 DB 721 GGATCTCCGCGAAAATGAATTCAAACAGATGCTGAATGCCAAACTCCCGATGGAGACC 780  
 QY 787 CCAGATTACATGCTCTGCTGAGTGTGATGAACGGGATGGAAGGACCACTAC 846  
 DB 781 CCAGATTACATGCTCTGCTGAGTGTGATGAACGGGATGGAAGGACCACTAC 840  
 QY 847 GGCCTGAGCTGTGATGCTGGTGTGAGTGGGCGTGTATGCTTATGAGATGATTTATGGAGA 906  
 DB 841 GGCCTGAGCTGTGATGCTGGTGTGAGTGGGCGTGTATGCTTATGAGATGATTTATGGAGA 900  
 QY 907 TCCCTCTCCGAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGATTTCCAGCGG 966  
 DB 901 TCCCTCTCCGAGAGGAACTCTGCGAGAACCTTCAATAACATTAATGATTTCCAGCGG 960  
 QY 967 TTTTGAATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026  
 DB 961 TTTTGAATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
 QY 1027 TTGTTGCGCGCAGAGAGAGACTGAAGTTTGAAGGCTTTTGTGCGCATCTCTTCTTC 1086  
 DB 1021 TTGTTGCGCGCAGAGAGAGACTGAAGTTTGAAGGCTTTTGTGCGCATCTCTTCTTC 1080  
 QY 1087 TCTAAAATTGACTGGAAACAACTTCTGTAACCTCTCTCCCTCTCTGTCACACCTCAAG 1146  
 DB 1081 TCTAAAATTGACTGGAAACAACTTCTGTAACCTCTCTCTCTCTCTGTCACACCTCAAG 1140  
 QY 1147 TCCGACGATGACACCTTCCAAATTTGATGAACACAGAGAAATTCGTGGGTTTCATCTCT 1206  
 DB 1141 TCTGACGATGACACCTTCCAAATTTGATGAACACAGAGAAATTCGTGGGTTTCATCTCT 1200  
 QY 1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGTAAGAACTGCGCTTGTGGGGTTTTCG 1266  
 DB 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGTAAGAACTGCGCTTGTGGGGTTTTCG 1260  
 QY 1267 TACAGCAAGCACTGGGGATTTCTGGTAGATCTGATCTGTTGTCGGGTCTGGACTCC 1326  
 DB 1261 TACAGCAAGCACTGGGGATTTCTGGTAGATCTGATCTGTTGTCGGGTCTGGACTCC 1320  
 QY 1327 CCTGCCAAGACTAGCTCCATGGAAGAACTTCTCATCAAGCAAGAGCTTACAGAC 1386  
 DB 1321 CCTGCCAAGACTAGCTCCATGGAAGAACTTCTCATCAAGCAAGAGCTTACAGAC 1380  
 QY 1387 TCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGAGCGCGCTCTCTCTGCTCCAGG 1446  
 DB 1381 TCTCAGGACAAAGTGTCAAGAGTATTTATTTCCGAGCGCGCTCTCTCTGCTCCAGG 1440  
 QY 1447 ATCTCTCCGCTCCGATATGCAAGGATCGCCCGGGCGGCTGC 1491  
 DB 1441 ATCTCTCCGCTCCGATATGCAAGGATCGCCCGGGCGGCTGC 1485

RESULT 7  
 AAD38864  
 ID AAD38864 standard; cDNA; 6298 BP.  
 XX  
 AC AAD38864;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human kinase (PKIN)-21 cDNA.  
 XX  
 KW Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;

KW	acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
KW	asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
KW	development; hepatitis; cardiovascular; hypertension; drug screening;
KW	myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
KW	fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
KW	hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-HIV;
KW	neuroprotective; hepatotropic; hypotensive; cardiac; nephrotropic;
KW	hyperlipidaemia; enzyme; gene; ss.
OS	Homo sapiens.
XX	
XX	Location/Qualifiers
XX	55..6219
FT	/*tag= a
FT	/product= "Human kinase (PKIN)-21"
XX	
XX	WO200233099-A2.
XX	
XX	25-APR-2002.
XX	
XX	20-OCT-2001; 2001WO-US047728.
XX	
XX	20-OCT-2000; 2000US-0242410P.
PR	27-OCT-2000; 2000US-0244068P.
PR	03-NOV-2000; 2000US-0245708P.
PR	09-NOV-2000; 2000US-0247672P.
PR	16-NOV-2000; 2000US-0249565P.
PR	22-NOV-2000; 2000US-0252730P.
PR	01-DEC-2000; 2000US-0250607P.
XX	
XX	(INCY-) INCYTE GENOMICS INC.
PA	
PI	Gururajan R, Baughn MR, Wallia NK, Elliott VS, Xu Y, Arvizu C;
PI	Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;
PI	Gandhi AS, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;
PI	Recipon SA, Lu DM, Borowsky ML, Thornton M, Swarnaker A;
PI	Thangavelu K, Khan FA, Ison CH;
XX	
XX	WPI; 2002-454603/48.
DR	P-PSDB; AA524150.
DR	
XX	
XX	New human kinase polypeptide, for diagnosing, preventing and treating
PT	cancer, immune system disorders, growth and development disorders,
PT	cardiovascular disorders and lipid disorders.
XX	
XX	Claim 5; Page 207-209; 210pp; English.
PS	
CC	The invention relates human kinases (PKIN) and their corresponding
CC	nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
CC	treating and preventing cancer, an immune system disorder (e.g., acquired
CC	immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
CC	atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC	growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC	cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC	Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC	Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
CC	hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC	compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC	condition or a disease associated with the expression of PKIN in a
CC	biological sample. A composition comprising PKIN or an agonist or
CC	antagonist of PKIN is useful for treating a disease or condition
CC	associated with decreased or increased expression of functional PKIN.
CC	PKIN is useful in a number of drug screening techniques and to analyse
CC	the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC	knockin humanised animals or transgenic animals to model human diseases,
CC	and in somatic or germline gene therapy. The present sequence is human
CC	PKIN cDNA
XX	
XX	Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;
SQ	
Query Match	92.7%; Score 1404.2; DB 6; Length 6298;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 1406; Conservative	0; Mismatches 3; Indels 0; Gaps 0;







QY 7 ATGTTGAGTTCAATATGAGCGCGGATCCTTTGGATGCTGGTGTCTGACCCCAAT 66  
DB |||||  
QY 14 ATGTTGAGTTCAATATGAGCGCGGATCCTTTGGATGCTGGTGTCTGACCCCAAT 73  
DB |||||  
QY 67 GCCAACCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCAA 126  
DB |||||  
QY 74 GCCAGCGGCGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCAACCTTTATGACTCAA 133  
DB |||||  
QY 127 CAGCAGATGCTCTCTCTTCCAGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186  
DB |||||  
QY 134 CAGCAGATGCTCTCTCTTCCAGAGAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 193  
DB |||||  
QY 187 GAATGCACTGAGCTGCTCTGATGAAGATTAGACACGTGAGCAACTTTGTCGGAAGTAT 246  
DB |||||  
QY 194 GAATGCACTGAGCTGCTCTGATGAAGATTAGACACGTGAGCAACTTTGTCGGAAGTAT 253  
DB |||||  
QY 247 TCCGACACCATGCTGAGTTACAGAGCTCAGCCTTCGGGAAAGGACTTTGAACTCAGA 306  
DB |||||  
QY 254 TCCGACACCATGCTGAGTTACAGAGCTCAGCCTTCGGGAAAGGACTTTGAACTCAGA 313  
DB |||||  
QY 307 AGTCTTGTAGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGG 366  
DB |||||  
QY 314 AGTCTTGTAGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCAACCGGG 373  
DB |||||  
QY 367 GACATCTATGCTATGAAGTGTATGAAGAGAGGCTTTATTGGCCCGAGAGCAGGTTTCA 426  
DB |||||  
QY 374 GACATCTATGCTATGAAGTGTATGAAGAGAGGCTTTATTGGCCCGAGAGCAGGTTTCA 433  
DB |||||  
QY 427 TTTTGTGAGGAGCGGAGACATATTATCTCGAAGCAGACAGCCCGTGGATCCCCCAATTA 486  
DB |||||  
QY 434 TTTTGTGAGGAGCGGAGACATATTATCTCGAAGCAGACAGCCCGTGGATCCCCCAATTA 493  
DB |||||  
QY 487 CAGTATGCTTTTCCAGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 546  
DB |||||  
QY 494 CAGTATGCTTTTCCAGACAAAATCACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 553  
DB |||||  
QY 547 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTTAGATGAACCACTGATACAGTTT 606  
DB |||||  
QY 554 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTTAGATGAACCACTGATACAGTTT 613  
DB |||||  
QY 607 TACCTAGCTGAGTGAATTTGGCTGTTCACAGCGTTTCATCTGATGGGATACGTGATCGA 666  
DB |||||  
QY 614 TACCTAGCTGAGTGAATTTGGCTGTTCACAGCGTTTCATCTGATGGGATACGTGATCGA 673  
DB |||||  
QY 667 GACATCAAGCTGAGAACATTTCTGTTGACCCGACAGGACACATCAAGCTGGTGAATTT 726  
DB |||||  
QY 674 GACATCAAGCTGAGAACATTTCTGTTGACCCGACAGGACACATCAAGCTGGTGAATTT 733  
DB |||||  
QY 727 GGATCTGCGCGAAGTGAATTCACACAGATGGTGAATGCCAATCCCGATTTGGGACC 786  
DB |||||  
QY 734 GGATCTGCGCGAAGTGAATTCACACAGATGGTGAATGCCAATCCCGATTTGGGACC 793  
DB |||||  
QY 787 CCAGATTACATGCTCCTGAGTGTGCTGATGAACGGGGATGGAAGGACACCTTAC 846  
DB |||||  
QY 794 CCAGATTACATGCTCCTGAGTGTGCTGATGAACGGGGATGGAAGGACACCTTAC 853  
DB |||||  
QY 847 GGCCTGGACTGATGCTGGTGTGCTGAGCGCGTATGGCTATGAGATGATTTATGGAGA 906  
DB |||||  
QY 854 GGCCTGGACTGATGCTGGTGTGCTGAGCGCGTATGGCTATGAGATGATTTATGGAGA 913  
DB |||||  
QY 907 TCCCTCTCCAGAGGGAACCTCTGCCAGAACCTTCAATAATATGAATTTCCAGCGG 966  
DB |||||  
QY 914 TCCCTCTCCAGAGGGAACCTCTGCCAGAACCTTCAATAATATGAATTTCCAGCGG 973  
DB |||||  
QY 967 TTTTGAATTTCCAGATGACCCCAAGGTGAGAGTGAATTTCTTGAATCTGATTCAAAGC 1026  
DB |||||  
QY 974 TTTTGAATTTCCAGATGACCCCAAGGTGAGAGTGAATTTCTTGAATCTGATTCAAAGC 1033  
DB |||||  
QY 1027 TTGTTGTGGCCAGAGGAGACTGAAGTTTGAAGGCTTTTGTGCTGCCATCTTTCTTC 1086  
DB |||||  
QY 1034 TTGTTGTGGCCAGAGGAGACTGAAGTTTGAAGGCTTTTGTGCTGCCATCTTTCTTC 1093  
DB |||||  
QY 1087 TCTAAATTTGACTGGAGAACAAATTCGTAACTCTCTCTCCCTCTGTTTCCACCCCTCAAG 1146  
DB |||||

DB 1094 TCTAAATTTGACTGGAGACACATTCGTAACTCTCTCTCCCTCTGTTCCACCTCAAG 1153  
QY 1147 TCCGACATGACACCTCCCAATTTTGTATGAACACAGAGAAATTCGTGGGTTTCATCTCT 1206  
DB 1154 TCTGACATGACACCTCCCAATTTTGTATGAACACAGAGAAATTCGTGGGTTTCATCTCT 1213  
QY 1207 CCGTGCAGCTGAGCCCTCAGCTTCTCGGTGAAGAACTGCGGTTTGTGGGTTTCG 1266  
DB 1214 CCGTGCAGCTGAGCCCTCAGCTTCTCGGTGAAGAACTGCGGTTTGTGGGTTTCG 1273  
QY 1267 TACAGCAAGCACTGGGGATTTCTGTAGATCTGAGTCTGTTGTGGTCTGGACTCC 1326  
DB 1274 TACAGCAAGCACTGGGGATTTCTGTAGATCTGAGTCTGTTGTGGTCTGGACTCC 1333  
QY 1327 CCGTGCAGCTGAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTTACAGAC 1386  
DB 1334 CCGTGCAGCTGAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTTACAGAC 1393  
QY 1387 TCTCAGGACAAAGTGTCAAAAGT 1409  
DB 1394 TCTCAGGACAAAGTGTCAAAAGT 1416  
  
RESULT 9  
ABQ78871  
ID ABQ78871 standard; cDNA; 5877 BP.  
XX  
AC ABQ78871;  
XX  
DT 10-OCT-2002 (first entry)  
DE Human kinase cDNA #2.  
KW Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;  
KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer;  
KW gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..5877  
FT /\*tag= a  
FT /product= "Kinase"  
XX  
XX WO200259325-A2.  
XX  
XX 01-AUG-2002.  
XX  
XX 20-DEC-2001; 2001WO-US050497.  
XX  
XX 27-DEC-2000; 2000US-0258335P.  
XX  
XX (LEXI-) LEXICON GENETICS INC.  
XX  
XX Yu X, Miranda M, Friddle CJ;  
XX  
XX WPI; 2002-599796/64.  
XX  
XX P-PSDB; ABB81928.  
XX  
XX Novel polynucleotide encoding human proteins that are structurally  
XX similar to animal kinases, useful for drug screening, diagnosis, in gene  
XX therapy of disorders and diseases e.g. cancer and pharmacogenomic  
XX applications.  
XX  
XX Disclosure; Page 44-45; 50pp; English.  
XX  
XX The invention relates to a novel human protein that shares structural  
XX similarity with animal kinases, including serine-threonine kinases,  
XX particularly Citron rho-interacting kinases. The proteins of the  
XX invention have nootropic and cytostatic activity. The polynucleotides may  
XX have a use in gene therapy. The encoded novel polypeptides are useful for  
XX generating antibodies, as reagents in diagnostic assays, for identifying

CC other cellular gene products related to NHP and as reagents in assays for  
 CC screening for compounds that are useful in the treatment of mental,  
 CC biological or medical disorders and diseases including cancer. The  
 CC sequence encodes a novel human kinase of the invention  
 XX  
 SQ Sequence 5877 BP; 1680 A; 1433 C; 1583 G; 1181 T; 0 U; 0 Other;

Query Match 92.3%; Score 1398.2; DB 6; Length 5877;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGTTGAAGTTCAATATGAGCGCGGAATCTTTGGATGCTGGTCTGCTGAACCCATT 66  
 DB 1 ATGTTGAAGTTCAATATGAGCGCGGAATCTTTGGATGCTGGTCTGCTGAACCCATT 60  
 QY 67 GCCAACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAACCAACCTTTATGACTCAA 126  
 DB 61 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTCCAGGGAACCAACCTTTATGACTCAA 120  
 QY 127 CAGCAGATGTCCTCTTTCCGGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 186  
 DB 121 CAGCAGATGTCCTCTTTCCGGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180  
 QY 187 GAATCAGTCAGCTGCTCTCATGAAGATTAAGCAGCTGAGCAACTTTGTCGGAAGTAT 246  
 DB 181 GAATCAGTCAGCTGCTCTCATGAAGATTAAGCAGCTGAGCAACTTTGTCGGAAGTAT 240  
 QY 247 TCCGACACCATGCTGAGTACAGAGCTCCAGCTTCGGCAAGGACTTCGAGTCTAGA 306  
 DB 241 TCCGACACCATGCTGAGTACAGAGCTCCAGCTTCGGCAAGGACTTCGAGTCTAGA 300  
 QY 307 AGTCTTTGAGTGTGGTCACTTTCTGCAAGTGCAGGTGTTAAGAGAGAAACCCGGG 366  
 DB 301 AGTCTTTGAGTGTGGTCACTTTCTGCTGAGTGCAGGTGTTAAGAGAGAAACCCGGG 360  
 QY 367 GACATCTATGCTATGAAGTATGAAGAGAGGCTTTATTTGGCCCGAGGAGCTTTCA 426  
 DB 361 GACATCTATGCTATGAAGTATGAAGAGAGGCTTTATTTGGCCCGAGGAGCTTTCA 420  
 QY 427 TTTTGTAGGAGAGCGGAAACATATTATCTCGAAGCAAGCCCGTGGATCCCCCAATTA 486  
 DB 421 TTTTGTAGGAGAGCGGAAACATATTATCTCGAAGCAAGCCCGTGGATCCCCCAATTA 480  
 QY 487 CAGTATGCTTTTCCAGCAAAATATCACTTTATCTGTCATGTAATATCAGCTTGGAGG 546  
 DB 481 CAGTATGCTTTTCCAGCAAAATATCACTTTATCTGTCATGTAATATCAGCTTGGAGG 540  
 QY 547 GACTTGCTGCTCACTTTGAATAGATATGAGGACCACTAGTGAAGAACCTGTATACAGTTT 606  
 DB 541 GACTTGCTGCTCACTTTGAATAGATATGAGGACCACTAGTGAAGAACCTGTATACAGTTT 600  
 QY 607 TACCTAGTGTGCTGANTTTGGCTGTTTCCAGAGCTTCTATCTGATGGGATACGTGCTATCGA 666  
 DB 601 TACCTAGTGTGCTGANTTTGGCTGTTTCCAGAGCTTCTATCTGATGGGATACGTGCTATCGA 660  
 QY 667 GACATCAGCTGTGAGCAATTTCTGTTGACCGCAGCAGACACATCAAGCTTGGATTTT 726  
 DB 661 GACATCAGCTGTGAGCAATTTCTGTTGACCGCAGCAGACACATCAAGCTTGGATTTT 720  
 QY 727 GGATCTGCCGCGAAATGAATTTCAAAACAAGATGCTGAATGCCAACTCCCGATTGGGACC 786  
 DB 721 GGATCTGCCGCGAAATGAATTTCAACAAGATGCTGAATGCCAACTCCCGATTGGGACC 780  
 QY 787 CCAGATTCATGGCTCTCTGAAGTCTGCTGATGTAAGACGGGATGAAAGGACCACTAC 846  
 DB 781 CCAGATTCATGGCTCTCTGAAGTCTGCTGATGTAAGACGGGATGAAAGGACCACTAC 840  
 QY 847 GGCCTGAGCTGTGATGCTGGTGTGCTGAGTGGCTGATTGCTCATGATGATGATTTATGGGAGA 906  
 DB 841 GGCCTGAGCTGTGATGCTGGTGTGCTGAGTGGCTGATTGCTCATGATGATGATTTATGGGAGA 900  
 QY 907 TCCGCCCTTCCAGAGGGAACCTTCCAGAACCTTCAATTAACATTTATGAATTTCCAGCGG 966

DB 901 TCCCCCTTCGACAGGGAACTCTGCGCAGAACCTTCAATTAACATTAATTAATTTCCAGCGG 960  
 QY 967 TTTTGAATTTTCCAGATGACCCCCAAAGTGAGCAGTGAATTTCTTGATCTGATTTCAAGC 1026  
 DB 961 TTTTGAATTTTCCAGATGACCCCCAAAGTGAGCAGTGAATTTCTTGATCTGATTTCAAGC 1020  
 QY 1027 TTGTTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTTGTGCGCATCTTTCTTC 1086  
 DB 1021 TTGTTGCGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTTGTGCGCATCTTTCTTC 1080  
 QY 1087 TCTAAATTTGACTGGAAACAACATTTCTAACTCTCTTCCCCCTTGGTCCCCACCTCAAG 1146  
 DB 1081 TCTAAATTTGACTGGAAACAACATTTCTAACTCTCTTCCCCCTTGGTCCCCACCTCAAG 1140  
 QY 1147 TCCGACGATGACACTTCCAAATTTTGAATGAACAGAGAGAAATTCGTGGTTCATCTCT 1206  
 DB 1141 TCTGACGATGACACTTCCAAATTTTGAATGAACAGAGAGAAATTCGTGGTTCATCTCT 1200  
 QY 1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGTGAAGAACTCCCGTTTGTGGGTTTTCG 1266  
 DB 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGTGAAGAACTCCCGTTTGTGGGTTTTCG 1260  
 QY 1267 TACAGCAAGGCACTGGGATTTCTGATAGATCTGATCTGTTGTCGCGTCTGAGTCC 1326  
 DB 1261 TACAGCAAGGCACTGGGATTTCTGATAGATCTGATCTGTTGTCGCGTCTGAGTCC 1320  
 QY 1327 CCGTGCAGCTGAGCTTCCATGGAAGAACTTCTCATMAAGCAAGAGCTACAAGAC 1386  
 DB 1321 CCGTGCAGCTGAGCTTCCATGGAAGAACTTCTCATMAAGCAAGAGCTACAAGAC 1380  
 QY 1387 TCTCAGGCAAGTGTCAAGGT 1409  
 DB 1381 TCTCAGGCAAGTGTCAAGAT 1403

RESULT 10  
 AAL55217  
 ID AAL55217 standard; DNA; 6156 BP.  
 XX  
 AC AAL55217;  
 XX  
 DT 01-MAY-2003 (first entry)  
 XX  
 DE Human CRK related DNA sequence, SEQ ID No 8.

XX Anorectic; hypotensive; cardiast; antilipemic; cerebroprotective;  
 KW antitumor; osteoplastic; antitumor; cytosolic; antidiabetic; antiparkinsonian; nootropic;  
 KW immunomodulator; antitumor; tranquilizer; antidiabetic; analgesic;  
 KW neuroprotective; antitumor; antidiabetic; antidiabetic; analgesic;  
 KW human citron rho/rac-interacting kinase; enzyme; CRK; ameliorating;  
 KW obesity; comorbidity; cancer; anorexia; cachexia; bulimia;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;  
 KW diabetes; pain; ds.

Homo sapiens.

WO200304523-A1.

16-JAN-2003.

28-JUN-2002; 2002WO-EP007156.

02-JUL-2001; 2001US-0301841P.

11-DEC-2001; 2001US-0338651P.

25-APR-2002; 2002US-0375014P.

(FARB ) BAYER AG.

Zhu Z;

WPI; 2003-221576/21.

New human citron rho/rac-interacting kinase (CRK) polypeptide and

polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CR1K dysfunction, e.g. obesity, diabetes or Alzheimer's disease.

Disclosure; Page 217-222; 237pp; English.

The invention relates to an isolated polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CR1K) polypeptide and polynucleotide are useful in preventing, ameliorating, or treating diseases associated with human CR1K dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer), anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's disease), chronic obstructive pulmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CR1K polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CR1K in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CR1K polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polynucleotide and polypeptide and in screening for agents that modulate the activity of the human CR1K polypeptide. This polynucleotide sequence represents a DNA sequence relating to the human CR1K protein of the invention

Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

Query Match 92.3%; Score 1398.2; DB 9; Length 6156;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

PT	polynucleotide, useful in preventing, ameliorating or treating diseases	
PT	associated with human CR1K dysfunction, e.g. obesity, diabetes or	
PT	Alzheimer's disease.	
XX		
PS	Disclosure; Page 217-222; 237pp; English.	
XX		
CC	The invention relates to an isolated polynucleotide encoding a human	
CC	citron rho/rac-interacting kinase polypeptide. The isolated	
CC	polynucleotide comprises a 6165 or 8603 base pair sequence, given in the	
CC	specification. The human citron rho/rac-interacting kinase (CR1K)	
CC	polypeptide and polynucleotide are useful in preventing, ameliorating, or	
CC	treating diseases associated with human CR1K dysfunction such as obesity	
CC	and obesity-associated comorbidities (e.g. hypertension, coronary artery	
CC	disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of	
CC	cancer including endometrial, breast, prostate and colon cancer),	
CC	anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood	
CC	disorders, anxiety disorders, Parkinson's disease or Alzheimer's	
CC	disease), chronic obstructive pulmonary disease, or diabetes. These can	
CC	also be used to treat pain associated with the disorders. The human CR1K	
CC	polypeptide is also useful in diagnostic assays or in genetic testing.	
CC	The expression vector or the reagent is useful in preparing a medicament	
CC	for modulating the activity of a human CR1K in a disease, e.g. obesity, a	
CC	central nervous system disorder, or chronic obstructive pulmonary	
CC	disease. The fusion protein is useful for generating antibodies against a	
CC	CR1K polypeptide and for use in various assay systems. The methods are	
CC	useful in producing and detecting the polynucleotide and polypeptide and	
CC	in screening for agents that modulate the activity of the human CR1K	
CC	polypeptide. This polynucleotide sequence represents a DNA sequence	
CC	relating to the human CR1K protein of the invention	
XX		
SQ	Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;	
Query Match	92.3%; Score 1398.2; DB 9; Length 6156;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 1400;	Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	7 ATGTTGAAGTTCAAATATGAGCGCGGAATCTTTGGATGCTGGTCTGTAACCCATT 66	
DB	1 ATGTTGAAGTTCAAATATGAGCGCGGAATCTTTGGATGCTGGTCTGTAACCCATT 60	
QY	67 GCCAACCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGAACACCCCTTATGACTCAA 126	
DB	61 GCCAGCGGCGCTCCAGGCTGAATCTGTTCTCCAGGGAACACCCCTTATGACTCAA 120	
QY	127 CAGCAGATGCTCTCTTCCGAGAGGGAATATAGATGCGCTCTTTCTCTTTGAA 186	
DB	121 CAGCAGATGCTCTCTTCCGAGAGGGAATATAGATGCGCTCTTTCTCTTTGAA 180	
QY	187 GAATGAGTCAGCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTCGCGAAGTAT 246	
DB	181 GAATGAGTCAGCTCTCTGATGAAGATTAAGCAGCTGAGCAACTTTCGCGAAGTAT 240	
QY	247 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGAGACTTCGAAGTCAGA 306	
DB	241 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAGAGACTTCGAAGTCAGA 300	
QY	307 AGTCTTGTAGTTGGTTCATCTTCTGAGTGCAGTCTGAGCAAGTTCGAGAGAACCCGG 366	
DB	301 AGTCTTGTAGTTGGTTCATCTTCTGAGTGCAGTCTGAGCAAGTTCGAGAGAACCCGG 360	
QY	367 GACATCTATGCTATGAAGTGTGAAGAGAGAGGCTTTTATGGCCAGGAGAGTTTCA 426	
DB	361 GACATCTATGCTATGAAGTGTGAAGAGAGAGGCTTTTATGGCCAGGAGAGTTTCA 420	
QY	427 TTTTGTGAGAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 486	
DB	421 TTTTGTGAGAGAGCGGAACATATATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 480	
QY	487 CAGTATGCTCTTTCAGGACAAAATACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 546	
DB	481 CAGTATGCTCTTTCAGGACAAAATACCTTTATCTGCTCATGGAATATCAGCTCGAGGG 540	
QY	547 GACTTGTGCTCACTTTTGAATAGATATGAGGACCACTTAGATGAAAAACCTGATACAGTTT 606	

RESULT 11

ABQ78870

ID ABQ78870 standard; cdna; 6165 BP.

XX ABQ78870;

XX 10-OCT-2002 (first entry)

XX Human kinase cdna #1.

XX Human; kinase; enzyme; serine-threonine kinase; neotrophic; cytostatic;  
XX Citron rho-interacting kinase; gene therapy; mental disorder; cancer;  
XX gene; ss.

DB	541 GACTTGTCTGTCATTTTGAATAGATATAGAGACGAGTTAGATGAAAAACCTGATACATTT 600	
QY	607 TACCTAGCTGAGCTGATTTTGGCTTGTTCACAGCGTTTCACTGATGGGATACGTGATCGA 666	
DB	601 TACCTAGCTGAGCTGATTTTGGCTTGTTCACAGCGTTTCACTGATGGGATACGTGATCGA 660	
QY	667 GACATCAAGCTGAGACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726	
DB	661 GACATCAAGCTGAGACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 720	
QY	727 GGATCTCCGCGCAAAATGAATTCAAAACAAGATGTTGAATGCAAACTCCGATTTGGAGC 786	
DB	721 GGATCTCCGCGCAAAATGAATTCAAAACAAGATGTTGAATGCAAACTCCGATTTGGAGC 780	
QY	787 CCAGATTACATGCTCTGCTGAGTCTGACTGTGTAACCGGGATGAAAAGGCACTAC 846	
DB	781 CCAGATTACATGCTCTGCTGAGTCTGACTGTGTAACCGGGATGAAAAGGCACTAC 840	
QY	847 GGCCTGCACTGTGACTGTGCTGAGTGGGCTGATTCGCTATGAGATGATTTATGGGAGA 906	
DB	841 GGCCTGCACTGTGACTGTGCTGAGTGGGCTGATTCGCTATGAGATGATTTATGGGAGA 900	
QY	907 TCCCTCTTCGAGAGGAACTCTGCCAGAACCTTCAATTAACATTAATTTCCAGCGG 966	
DB	901 TCCCTCTTCGAGAGGAACTCTGCCAGAACCTTCAATTAACATTAATTTCCAGCGG 960	
QY	967 TTTTGTAAATTTCCAGATGACCCCAAGTGAAGTCACTTTCTTTGATCTGATTTCAAGC 1026	
DB	961 TTTTGTAAATTTCCAGATGACCCCAAGTGAAGTCACTTTCTTTGATCTGATTTCAAGC 1020	
QY	1027 TTGTTGTGCGCCAGAGAGAGACTGAAATTTGAAGTCTTTGCTGCCATTCCTTCTTC 1086	
DB	1021 TTGTTGTGCGCCAGAGAGAGACTGAAATTTGAAGTCTTTGCTGCCATTCCTTCTTC 1080	
QY	1087 TCTAAATTTGACTCGAACACATTCGTAACCTCTCCCTCCCTTCGTTCCCACTCAAG 1146	
DB	1081 TCTAAATTTGACTCGAACACATTCGTAACCTCTCCCTCCCTTCGTTCCCACTCAAG 1140	
QY	1147 TCCAGCATGACACTCCAAATTTTGAAGTGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1206	
DB	1141 TCTAGCATGACACTCCAAATTTTGAAGTGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1200	
QY	1207 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGTGAAGAACTGCGGTTTGGGGTTTTCG 1266	
DB	1201 CCGTCCAGCTGAGCCCTCAGGCTTCTCGGTGAAGAACTGCGGTTTGGGGTTTTCG 1260	
QY	1267 TACAGAGGCACTGGGATTTCTTGTAGATCTGAGTCTGTTGTGCGGTTCTGAGTCTC 1326	
DB	1261 TACAGAGGCACTGGGATTTCTTGTAGATCTGAGTCTGTTGTGCGGTTCTGAGTCTC 1320	
QY	1327 CCTGCCAAGACTAGCTCCATGGAAGAAATCTTCTCATTAAGCAAGAGCTACAGAC 1386	
DB	1321 CCTGCCAAGACTAGCTCCATGGAAGAAATCTTCTCATTAAGCAAGAGCTACAGAC 1380	
QY	1387 TCTCAGAGCAAGTGTCAAGGT 1409	
DB	1381 TCTCAGAGCAAGTGTCAAGAT 1403	

XX OS Homo sapiens.  
 XX PH Key  
 XX FT CDS  
 XX FT Location/Qualifiers  
 XX FT 1. .6165  
 XX FT /tag= a "Kinase"  
 XX FT /product= "Kinase"  
 XX FT replace(5218,G)  
 XX FT /tag= b  
 XX FT /standard\_name= "Single nucleotide polymorphism"  
 XX FT replace(6065,G)  
 XX FT /tag= b  
 XX FT /standard\_name= "Single nucleotide polymorphism"  
 XX PN WO200259325-A2.  
 XX XX  
 XX PD 01-AUG-2002.  
 XX XX  
 XX PF 20-DEC-2001; 2001WO-US050497.  
 XX XX  
 XX PR 27-DEC-2000; 2000US-0259335P.  
 XX XX  
 XX PA (LEXI-) LEXICON GENETICS INC.  
 XX XX  
 XX PI Yu X, Miranda M, Fiddle CJ;  
 XX XX  
 XX DR WPI: 2002-599796/64.  
 XX DR P-PSDB; ABB81927.  
 XX XX  
 XX PT Novel polynucleotide encoding human proteins that are structurally  
 XX PT similar to animal kinases, useful for drug screening, diagnosis, in gene  
 XX PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
 XX PT applications.  
 XX XX  
 XX PS Claim 1; Page 37-39; 50pp; English.  
 XX XX  
 XX CC The invention relates to a novel human protein that shares structural  
 XX CC similarity with animal kinases, including serine-threonine kinases,  
 XX CC particularly Citron rho-interacting kinases. The proteins of the  
 XX CC invention have nontropic and cytosolic activity. The polynucleotides may  
 XX CC have a use in gene therapy. The encoded novel polypeptides are useful for  
 XX CC generating antibodies, as reagents in diagnostic assays, for identifying  
 XX CC other cellular gene products related to NHP and as reagents in assays for  
 XX CC screening for compounds that are useful in the treatment of mental,  
 XX CC biological or medical disorders and diseases including cancer. The  
 XX CC sequence encodes a novel human kinase of the invention  
 XX XX  
 XX SQ Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;  
 XX XX  
 XX Query Match 92.3%; Score 1398.2; DB 6; Length 6165;  
 XX Best Local Similarity 99.8%; Pred. No. 0;  
 XX Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 ATGTTGAAGTCAATATGAGCGCGGAATCCTTTGGATGCTGGTGTGCTGAACCCATT 66  
 DB 1 ATGTTGAAGTCAATATGAGCGCGGAATCCTTTGGATGCTGGTGTGCTGAACCCATT 60  
 QY 67 GCCAACCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 126  
 DB 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 120  
 QY 127 CAGCAGATGCTCCTCTTCCGGAAGGATATTAGATGCCCTTTGTTCTCTTTGAA 186  
 DB 121 CAGCAGATGCTCCTCTTCCGGAAGGATATTAGATGCCCTTTGTTCTCTTTGAA 180  
 QY 187 GAATCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTTGTCGGAATAT 246  
 DB 181 GAATCAGTCAAGCTGCTCTGATGAAGATTAAAGCAGTGAACAACTTTGTCGGAATAT 240  
 QY 247 TCCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGGAAGGACTTCGAGTCTAGA 306  
 DB 241 TCCGACACCATAGCTGAGTTACAGAGCTTCAGGCTTCGGAAGGACTTCGGAAGTCTAGA 300

QY 307 AGTCTTGTAGTGTGCTGCTACCTTTGCTGAAGTCAGGCTGTGAAGAGAAAGCAACCCGG 366  
 DB 301 AGTCTTGTAGTGTGCTGCTACCTTTGCTGAAGTCAGGCTGTGAAGAGAAAGCAACCCGG 360  
 QY 367 GACATCTATGCTATGAAAGTGAAGAGAGAGGCTTTATTTGGCCCGAGGAGGTTTCA 426  
 DB 361 GACATCTATGCTATGAAAGTGAAGAGAGAGGCTTTATTTGGCCCGAGGAGGTTTCA 420  
 QY 427 TTTTGTGAGAGAGCGGAAACATATTATCTGAGACAAAGCCCGTGGATCCCCCAATTA 486  
 DB 421 TTTTGTGAGAGAGCGGAAACATATTATCTCGAAGACAAAGCCCGTGGATCCCCCAATTA 480  
 QY 487 CAGTATGCTCTTCAGGACAAAAATCACTTTATCTGCTCATGGAATATCAGCTCGAGGG 546  
 DB 481 CAGTATGCTCTTCAGGACAAAAATCACTTTATCTGCTCATGGAATATCAGCTCGAGGG 540  
 QY 547 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTTAGATGAATAACCTGTATACGTTT 606  
 DB 541 GACTTGTCTCACTTTTGAATAGATATGAGGACCACTTAGATGAATAACCTGTATACGTTT 600  
 QY 607 TACCTAGCTGAGCTGATTTTGGCTGTTACAGGTTTCATCTGATGGATACGTCATCGA 666  
 DB 601 TACCTAGCTGAGCTGATTTTGGCTGTTACAGGTTTCATCTGATGGATACGTCATCGA 660  
 QY 667 GACATCAAGCTCAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTT 726  
 DB 661 GACATCAAGCTCAGAAACATTTCTGTTGACCGCACAGGACACATCAAGCTGGTGGATTT 720  
 QY 727 GATCTGCGCGGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCGATTTGGGACC 786  
 DB 721 GATCTGCGCGGAAATGAATTCAAACAGATGGTGAATGCCAAACTCCGATTTGGGACC 780  
 QY 787 CCAGATTACATGCTCTCTGAGTGTGCTGATGAACGGGATGGAAGGCACTTAC 846  
 DB 781 CCAGATTACATGCTCTCTGAGTGTGCTGATGAACGGGATGGAAGGCACTTAC 840  
 QY 847 GGCTGAGCTGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 906  
 DB 841 GGCTGAGCTGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900  
 QY 907 TCCCTCTTCGAGAGGAACTCTGCGAGAACTCTCAATAAATATGAATTTCCAGCGG 966  
 DB 901 TCCCTCTTCGAGAGGAACTCTGCGAGAACTCTCAATAAATATGAATTTCCAGCGG 960  
 QY 967 TTTTGAATTTCCAGATCAACCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1026  
 DB 961 TTTTGAATTTCCAGATCAACCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020  
 QY 1027 TTGTTGCGGCGCAGAAAGAGAGAGCTGAAGTTTGAAGTGGTGGTGGTGGTGGTGGTGGTGG 1086  
 DB 1021 TTGTTGCGGCGCAGAAAGAGAGAGCTGAAGTTTGAAGTGGTGGTGGTGGTGGTGGTGGTGG 1080  
 QY 1087 TCTAAATTTGACTGGAACCAACATTTGCTAACTCTCTCTCCCTCCCTCTCTCCCTCCCTCAAG 1146  
 DB 1081 TCTAAATTTGACTGGAACCAACATTTGCTAACTCTCTCTCCCTCCCTCTCTCTCCCTCAAG 1140  
 QY 1147 TCCGACGATGACACCTCCAAATTTTGAATGAACAGAGAGAGAGTTCGTTGGTTCATCTCT 1206  
 DB 1141 TCTGACGATGACACCTCCAAATTTTGAATGAACAGAGAGAGAGTTCGTTGGTTCATCTCT 1200  
 QY 1207 CCGTGCAGCTGAGCCCTCAGGCTTTCTCGGCTGAAGAACTCCCTTTTGTGGGGTTTTGCG 1266  
 DB 1201 CCGTGCAGCTGAGCCCTCAGGCTTTCTCGGCTGAAGAACTCCCTTTTGTGGGGTTTTGCG 1260  
 QY 1267 TACAGAAAGGCACTGGGATTTCTTGTAGATCTGAGTCTGTTGTGTCGGGTCTGAGTCC 1326  
 DB 1261 TACAGAAAGGCACTGGGATTTCTTGTAGATCTGAGTCTGTTGTGTCGGGTCTGAGTCC 1320  
 QY 1327 CCGTGCAGCTGAGCTCCATGGAAGAACTTTCTCATCAAAAGCAAGAGCTTCAAGAC 1386  
 DB 1321 CCGTGCAGCTGAGCTCCATGGAAGAACTTTCTCATCAAAAGCAAGAGCTTCAAGAC 1380  
 QY 1387 TCTCAGGACAAAGTGTCTCAAGGT 1409



Db 901 TCCCCCTTCGACAGAGGAACCTCTGCCAGAACCTTCAATAACATPATGAATTCACGGG 960  
 Qy 967 TTTTGTGAATTTCCAGATGACCCCAAGAGTACGAGTCTTTCTGATCTGATTCAGAGC 1026  
 Db 961 TTTTGTGAATTTCCAGATGACCCCAAGAGTACGAGTCTTTCTGATCTGATTCAGAGC 1020  
 Qy 1027 TTTTGTGGGCGCAGAAAGAGAGCTGAAGTTTGAAGTCTTTGTGTCATCTTTTC 1086  
 Db 1021 TTTTGTGGGCGCAGAAAGAGAGCTGAAGTTTGAAGTCTTTGTGTCATCTTTTC 1080  
 Qy 1087 TCTAATTAATGACTGGACACAACTGTAAGTCTCTCCCTTCTGTTCCACCTCAAG 1146  
 Db 1081 TCTAATTAATGACTGGACACAACTGTAAGTCTCTCCCTTCTGTTCCACCTCAAG 1140  
 Qy 1147 TCCGAGATGACACCTCCCAATTTTGTATGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1206  
 Db 1141 TCTGACGATGACACCTCCCAATTTTGTATGAACAGAGAGAAATTCGTGGGTTTCATCTCT 1200  
 Qy 1207 CGTGCCAGCTAGCCCTCAGCTTCTCGGCTGAGAACTCCCTTTGTGGGTTTCG 1266  
 Db 1201 CGTGCCAGCTAGCCCTCAGCTTCTCGGCTGAGAACTCCCTTTGTGGGTTTCG 1260  
 Qy 1267 TACAGCAAGCACTGGGATCTTGTAGATCTGATCTGTTGTGCGGGTCTGGACTCC 1326  
 Db 1261 TACAGCAAGCACTGGGATCTTGTAGATCTGATCTGTTGTGCGGGTCTGGACTCC 1320  
 Qy 1327 CTTGCCAAGACTAGCTTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTACAAG 1386  
 Db 1321 CTTGCCAAGACTAGCTTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTACAAG 1380  
 Qy 1387 TCTCAGCAAGTGTCAACAGGT 1409  
 Db 1381 TCTCAGCAAGTGTCAACAGAT 1403

RESULT 13  
 AAL55215  
 ID AAL55215 standard; DNA; 8603 BP.  
 XX AAL55215;  
 AC AAL55215;  
 DT 01-MAY-2003 (first entry)  
 XX Human CRUK related DNA sequence, SEQ ID No 4.  
 DE Anorectic; hypotensive; cardiac; antilipemic; cerebroprotective;  
 XX antitumor; osteopathic; antiarthritic; cytosolic; antidepressant;  
 KW immunomodulator; antitumor; tranquilizer; antiparkinsonian; nootropic;  
 KW neuroprotective; antiinflammatory; antidiabetic; analgesic;  
 KW human citron rho/rac-interacting kinase; enzyme; CRUK; ameliorating;  
 KW obesity; comorbidities; cancer; anorexia; cachexia; bulimia;  
 KW central nervous system disorder; chronic obstructive pulmonary disease;  
 KW diabetes; pain; ds.  
 XX Homo sapiens.  
 OS WO2003004523-A1.  
 XX 16-JAN-2003.  
 XX 28-JUN-2002; 2002WO-BP007156.  
 XX 02-JUL-2001; 2001US-0301841P.  
 PR 11-DEC-2001; 2001US-0338651P.  
 PR 25-APR-2002; 2002US-0375014P.  
 XX (FARB ) BAYER AG.  
 PA Zhu Z;  
 XX WPI; 2003-221576/21.  
 DR New human citron rho/rac-interacting kinase (CRUK) polypeptide and

PT polynucleotide, useful in preventing, ameliorating or treating diseases  
 PT associated with human CRUK dysfunction, e.g. obesity, diabetes or  
 XX Alzheimer's disease.  
 PS Disclosure; Fig 4; 237pp; English.  
 XX The invention relates to an isolated polynucleotide encoding a human  
 CC citron rho/rac-interacting kinase polypeptide. The isolated  
 CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the  
 CC specification. The human citron rho/rac-interacting kinase (CRUK)  
 CC polypeptide and polynucleotide are useful in preventing, ameliorating, or  
 CC treating diseases associated with human CRUK dysfunction such as obesity  
 CC and obesity-associated comorbidities (e.g. hypertension, coronary artery  
 CC disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of  
 CC cancer including endometrial, breast, prostate and colon cancer),  
 CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood  
 CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's  
 CC disease), chronic obstructive pulmonary disease, or diabetes. These can  
 CC also be used to treat pain associated with the disorders. The human CRUK  
 CC polypeptide is also useful in diagnostic assays or in genetic testing.  
 CC The expression vector or the reagent is useful in preparing a medicament  
 CC for modulating the activity of a human CRUK in a disease, e.g. obesity, a  
 CC central nervous system disorder, or chronic obstructive pulmonary  
 CC disease. The fusion protein is useful for generating antibodies against a  
 CC CRUK polypeptide and for use in various assay systems. The methods are  
 CC useful in producing and detecting the polynucleotide and polypeptide and  
 CC in screening for agents that modulate the activity of the human CRUK  
 CC polypeptide. This polynucleotide sequence represents a DNA sequence  
 CC relating to the human CRUK protein of the invention  
 XX  
 Qy Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other;  
 Query Match 92.3%; Score 1398.2; DB 9; Length 8603;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 7 ATGTTGAAGTTCAAATATGAGCGCGGAATCTTTGGATGCTGGTCTCTGAACCCATT 66  
 Db 1 ATGTTGAAGTTCAAATATGAGCGCGGAATCTTTGGATGCTGGTCTCTGAACCCATT 60  
 Qy 67 GCCAACCGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCCTTTAGTCTCA 126  
 Db 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCCCTTTAGTCTCA 120  
 Qy 127 CAGCAGATGCTCTCTTTCCGAGAGGATATTAGATGCCCTCTTTCTCTTTGAA 186  
 Db 121 CAGCAGATGCTCTCTTTCCGAGAGGATATTAGATGCCCTCTTTCTCTTTGAA 180  
 Qy 187 GAATGAGTCAAGCTCTGATGAAGATTAAACGCTGAGCAACTTTGTCGGAGATAT 246  
 Db 181 GAATGAGTCAAGCTCTGATGAAGATTAAACGCTGAGCAACTTTGTCGGAGATAT 240  
 Qy 247 TCCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGCAAGGACTTCGAAGTCAGA 306  
 Db 241 TCCGACACCATAGCTGAGTTACAGAGCTCCAGCTTCGCAAGGACTTCGAAGTCAGA 300  
 Qy 307 AGTCTTGTAGTTGTGGTCACTTTTGTGAGTGCAGTGGTGAAGAGAAAGCAACCGG 366  
 Db 301 AGTCTTGTAGTTGTGGTCACTTTTGTGAGTGCAGTGGTGAAGAGAAAGCAACCGG 360  
 Qy 367 GACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGCCCCAGGAGGTTTCA 426  
 Db 361 GACATCTATGCTATGAAGTGAAGAGAGGCTTTATTTGCCCCAGGAGGTTTCA 420  
 Qy 427 TTTTGTGAGGAGAGCGGAACATATTATCTCGAAGCAAGCCCGTGGATCCCCCAATTA 486  
 Db 421 TTTTGTGAGGAGAGCGGAACATATTATCTCGAAGCAAGCCCGTGGATCCCCCAATTA 480  
 Qy 487 CAGTATGCTCTTTCAGACAAATATCACTTTATCTGTCATGGAATATCAGCTCGAGG 546  
 Db 481 CAGTATGCTCTTTCAGACAAATATCACTTTATCTGTCATGGAATATCAGCTCGAGG 540  
 Qy 547 GACTTGTGTCACCTTTTGAATAGATATGAGGACCACTAGATGAAAAACCTGATACAGTTT 606

Db 541 GACTTGCTGACATTTTGAATAGATATGAGGACCAAGTTAGTAAAAACCTGTACAGTTT 600  
 Qy 607 TACCTAGCTGAGTGTATTTGGCTGTTTCACAGGTTTCATCTGATGGGATACGTCATCGA 666  
 Db 601 TACCTAGCTGAGTGTATTTGGCTGTTTCACAGGTTTCATCTGATGGGATACGTCATCGA 660  
 Qy 667 GACATCAAGCTGAGAACATCTCTGTTGACCGACAGGACACATCAAGCTGTGGATTTT 726  
 Db 661 GACATCAAGCTGAGAACATCTCTGTTGACCGACAGGACACATCAAGCTGTGGATTTT 720  
 Qy 727 GGATCTCCGCGAAATGTAATCAACAAGATGGTGAATCCAACTCCGATTTGGGACC 786  
 Db 721 GGATCTCCGCGAAATGTAATCAACAAGATGGTGAATCCAACTCCGATTTGGGACC 780  
 Qy 787 CCAGATTACATGCTCTCTGAAGTCTGACTGTGATGAACGGGATGAAAAAGGCACCTAC 846  
 Db 781 CCAGATTACATGCTCTCTGAAGTCTGACTGTGATGAACGGGATGAAAAAGGCACCTAC 840  
 Qy 847 GGCCTGAGCTGACTGGTGGTCACTGGGCGTGAATTCCTATGAGATGATTTATGGGAGA 906  
 Db 841 GGCCTGAGCTGACTGGTGGTCACTGGGCGTGAATTCCTATGAGATGATTTATGGGAGA 900  
 Qy 907 TCCCCCTTCCAGAGGAACTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 966  
 Db 901 TCCCCCTTCCAGAGGAACTCTGCCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 960  
 Qy 967 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTTCAAAGC 1026  
 Db 961 TTTTGAATTTCCAGATGACCCCAAGTGAGCAGTGACTTTCTTGATCTGATTTCAAAGC 1020  
 Qy 1027 TTGTTGTGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC 1086  
 Db 1021 TTGTTGTGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTTGCTGCCATCCTTTCTTC 1080  
 Qy 1087 TCTAAAATTGACTGGAACAACATTCGTAATCTCTCCCTCCCTTCTGTTCCACCTCAAG 1146  
 Db 1081 TCTAAAATTGACTGGAACAACATTCGTAATCTCTCCCTCCCTTCTGTTCCACCTCAAG 1140  
 Qy 1147 TCCGAGCATGACACTCCCAATTTTGTATGACACAGAGAAATTCGTGGTTTCATCCTCT 1206  
 Db 1141 TCGAGCATGACACTCCCAATTTTGTATGACACAGAGAAATTCGTGGTTTCATCCTCT 1200  
 Qy 1207 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGTTTCTGGGGTTTTCG 1266  
 Db 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCGTTTCTGGGGTTTTCG 1260  
 Qy 1267 TACAGCAAGCACTGGGATTTCTTGTAGATCTGTTGTGTCGGTCTGAGCTCC 1326  
 Db 1261 TACAGCAAGCACTGGGATTTCTTGTAGATCTGTTGTGTCGGTCTGAGCTCC 1320  
 Qy 1327 CCTGCCAAGACTAGCTCCATGAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1386  
 Db 1321 CCTGCCAAGACTAGCTCCATGAAAGAACTTCTCATCAAAAGCAAGAGCTACAAGAC 1380  
 Qy 1387 TCTCAGGACAAGTGTCAAGGT 1409  
 Db 1381 TCTCAGGACAAGTGTCAAGAT 1403

RESULT 14

AAD39191  
 ID AAD39191 standard; cDNA; 6574 BP.  
 XX  
 AC AAD39191;  
 XX  
 DT 04-OCT-2002 (first entry)  
 XX  
 DE Human MDPK cDNA.  
 XX  
 KW Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein;  
 KW tumorigenesis; tumor growth; tumor metastasis; viral infection;  
 KW skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;

immune disorder; neoplastic disorder; gene therapy; gene; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 5'UTR 1..18  
 FT /\*tag= a  
 FT 19..6180  
 FT /\*tag= b  
 FT /\*product= "Human MDPK protein"  
 FT 19..6177  
 FT /\*tag= c  
 FT /\*note= "This region is specifically referred in claim 1  
 as SEQ ID NO:3"  
 FT 6181..6574  
 FT /\*tag= d  
 FT  
 FT  
 XX  
 PN WO200234896-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 23-OCT-2001; 2001WO-US050636.  
 XX  
 PR 23-OCT-2000; 2000US-0242429P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Kapeller-Libermann R;  
 XX  
 DR WPI; 2002-479720/51.  
 DR P-PSDB; AAE24079.  
 XX  
 PT Human myotonic dystrophy type protein kinase polypeptide and  
 PT polynucleotide useful for prognosticating, diagnosing, preventing or  
 PT inhibiting tumorigenesis, tumor growth, tumor metastasis and viral  
 PT infection.  
 XX  
 PS Claim 1; Fig 1; 148pp; English.  
 XX  
 CC The invention relates to human myotonic dystrophy type protein kinase  
 CC (MDPK) polypeptides designated as 13245 and nucleic acid molecules  
 CC encoding such polypeptides. 13245 molecules are used to develop  
 CC diagnostic and therapeutic agents for prognosticating, diagnosing,  
 CC preventing, inhibiting, alleviating or curing MDPK-related disorders.  
 CC Polypeptides of the invention are used to develop diagnostic and  
 CC therapeutic agents for 13245-mediated or related disorders such as  
 CC tumorigenesis, tumor growth, tumor metastasis, viral infection of a  
 CC cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),  
 CC immune disorders and neoplastic disorders. The invention is also used in  
 CC gene therapy. The present sequence is human MDPK cDNA  
 XX  
 SQ Sequence 6574 BP; 1977 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;  
 Query Match 92.3%; Score 1397.8; DB 6; Length 6574;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 GGGGAGATGTGAAGTTCAAAATATGGAGCGCGGAATCTTTGGATGCTGCTGTGAA 60  
 Db 13 GGGGAGATGTGAAGTTCAAAATATGGAGCGCGGAATCTTTGGATGCTGCTGTGAA 72  
 Qy 61 CCCATTGCCAACCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 120  
 Db 73 CCCATTGCCAGCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACACCCCTTTATG 132  
 Qy 121 ACTCAACAGCAGATGCTCTCTTTTCCGAGAGAGGATATTAGATGCCCTTTTGTCTC 180  
 Db 133 ACTCAACAGCAGATGCTCTCTCTTTTCCGAGAGAGGATATTAGATGCCCTTTTGTCTC 192  
 Qy 181 TTTGAAGAATGCACTGAGCTGCTCTGATGAAGATTAAGCACGTCGAGCACTTTGTCGG 240  
 Db 193 TTTGAAGAATGCACTGAGCTGCTCTGATGAAGATTAAGCACGTCGAGCACTTTGTCGG 252



QY	241	AA	GTATTTCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTTCGGCAAAAGGACTTTCGAA	300
Db	253	AA	GTATTTCCGACACCATAGCTGAGTTTACAGGAGCTCCAGCCTTTCGGCAAAAGGACTTTCGAA	312
QY	301	GT	CAGAAGTCTTGTAGTGTGGTCTACTTTGCTGAAGTGCAGGTGTTAAGAGAGAAGCA	360
Db	313	GT	CAGAAGTCTTGTAGTGTGGTCTACTTTGCTGAAGTGCAGGTGTTAAGAGAGAAGCA	372
QY	361	AC	CGGGGACATCTATGCTATGAAAGTGATCAAGAAGAGGCTTTATTTGGCCCGAGGACGAG	420
Db	373	AC	CGGGGACATCTATGCTATGAAAGTGATCAAGAAGAGGCTTTATTTGGCCCGAGGACGAG	432
QY	421	GT	TTTCAATTTTTGAGGAAGCGGAAACATATTTATCTCGAAGCACAAGCCCGTGGATCCCC	480
Db	433	GT	TTTCAATTTTTGAGGAAGCGGAAACATATTTATCTCGAAGCACAAGCCCGTGGATCCCC	492
QY	481	CA	ATTACAGTATCCCTTTTCAGGCAAAAATTCACCTTTATCTGGTCAATGAATATCAGCCT	540
Db	493	CA	ATTACAGTATCCCTTTTCAGGCAAAAATTCACCTTTATCTGGTCAATGAATATCAGCCT	552
QY	541	GG	AGGGGACTTGCTGTCACTTTTGAATPAGATATGAGGACCGATTAGATGAACACCTTGATA	600
Db	553	GG	AGGGGACTTGCTGTCACTTTTGAATPAGATATGAGGACCGATTAGATGAACACCTTGATA	612
QY	601	CAG	TTTACCTAGCTGAGCTGATTTTGGCTGTTTCAGCGTTTCATCTGATGGATACGTCG	660
Db	613	CAG	TTTACCTAGCTGAGCTGATTTTGGCTGTTTCAGCGTTTCATCTGATGGATACGTCG	672
QY	661	CAT	CGAGACATCAAGCCTGAGAACATTTCTCGTTGACCGCAAGGACACATCAAGCTGGTG	720
Db	673	CAT	CGAGACATCAAGCCTGAGAACATTTCTCGTTGACCGCAAGGACACATCAAGCTGGTG	732
QY	721	GAT	TTTGGATCTGCGCGAANAATGAATTCAAAACAAGTGGTGAATCCCAACTCCCGATT	780
Db	733	GAT	TTTGGATCTGCGCGAANAATGAATTCAAAACAAGTGGTGAATCCCAACTCCCGATT	792
QY	781	GG	CAACCCAGATTACATGGCTCTCTGAAGTCTGACTGTGATGAACCGGGATGAAAAGGC	840
Db	793	GG	CAACCCAGATTACATGGCTCTCTGAAGTCTGACTGTGATGAACCGGGATGAAAAGGC	852
QY	841	AC	CTAGCGCTGAGCTGTGACTGGTGTGAGTGGGCGTGAATGCCCTATGAGATGATTTAT	900
Db	853	AC	CTAGCGCTGAGCTGTGACTGGTGTGAGTGGGCGTGAATGCCCTATGAGATGATTTAT	912
QY	901	GG	GAGATCTCCCTTTTCGACAGGGAACCTCTGCACAGACCTTCAATAACAATATGAATTC	960
Db	913	GG	GAGATCTCCCTTTTCGACAGGGAACCTCTGCACAGACCTTCAATAACAATATGAATTC	972
QY	961	CAG	CGTTTGTGAATTTCCAGATGACCCCAAAAGTGAAGAGTGAATCTTCTGATCTGATT	1020
Db	973	CAG	CGTTTGTGAATTTCCAGATGACCCCAAAAGTGAAGAGTGAATCTTCTGATCTGATT	1032
QY	1021	CA	AAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAAGTTCAAGGTCTTTCTGCCATCCT	1080
Db	1033	CA	AAAGCTTGTGTGCGGCCAGAAAGAGAGACTGAAAGTTCAAGGTCTTTCTGCCATCCT	1092
QY	1081	TT	CTCTCTCTAAAATTGACTGGAAACAACATTCGTAACTCTCTCTCCCTTCGTTGCCACC	1140
Db	1093	TT	CTCTCTCTAAAATTGACTGGAAACAACATTCGTAACTCTCTCTCCCTTCGTTGCCACC	1152
QY	1141	CT	CAAGTCCGACGATGACCTCCAAATTTTGATGAACACAGAGAAGAAATTCGTGGGTTCA	1200
Db	1153	CT	CAAGTCTGACGATGACCTCCAAATTTTGATGAACACAGAGAAGAAATTCGTGGGTTCA	1212
QY	1201	TC	CTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTCCCGTTTGTGGG	1260
Db	1213	TC	CTCTCCGTCGACGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTCCCGTTTGTGGG	1272
QY	1261	TTTT	TCGTACAGCAAGCACTGGGATTCCTGGTGAATCTCAGTCTGTTGTCTGGGCTG	1320
Db	1273	TTTT	TCGTACAGCAAGCACTGGGATTCCTGGTGAATCTCAGTCTGTTGTCTGGGCTG	1332
QY	1321	GACT	CCCTCTGCAAGACTAGCTCCATCGAAAAGAAATCTTCATCAAAAGCAAGAGCTA	1380

Db	1333	GACTCCCTGCGCAAGACTAGCTCCATGTAAGAAACCTTCTCATCAAAAGCAAGAGCTA	1392
Qy	1381	CAAGACTCTCAGGACAAAGTGTCACAAGGT	1409
Db	1393	CAAGACTCTCAGGACAAAGTGTCACAAGAT	1421
RESULT 15			
ADPF60992			
ID	ADPF60992	standard; DNA; 6574 BP.	
AC	ADPF60992;		
XX	XX		
DT	12-FEB-2004	(first entry)	
XX	XX		
DE	DE	Pain associated human 2207 gene.	
XX	XX		
KW	KW	Pain modulation; pain disorder; painful disorder; potassium channel;	
XX	XX	kinase expression; inflammatory pain; chronic pain; neuropathic pain;	
KW	KW	causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;	
XX	XX	analgesic; antiinflammatory; gene; ds.	
OS	OS	Homo sapiens.	
XX	XX		
US	US	US2003153525-A1.	
PN	PN		
XX	XX	14-AUG-2003.	
PD	PD		
XX	XX	19-DEC-2002; 2002US-00325430.	
XX	XX		
PR	PR	19-DEC-2001; 2001US-0341953P.	
XX	XX	(MILL-) MILLENNIUM PHARM INC.	
PA	PA		
XX	XX	Silos-Santiago I, Rosenfeld JB;	
PI	PI		
XX	XX	WPI; 2003-897732/82.	
DR	DR	P-PSDB; ADF60994.	
DR	DR		
XX	XX		
PT	PT	Identifying a compound capable of treating a pain disorder comprises	
PT	PT	assaying the ability of the compound to modulate specific e.g., kinases	
PT	PT	or potassium channel, nucleic acid expression or polypeptide activities.	
XX	XX		
PS	PS	Disclosure; SEQ ID NO 10; 80pp; English.	
XX	XX		
CC	CC	The present invention relates to a method for identifying a compound	
CC	CC	capable of modulating pain or painful disorders. The method comprises	
CC	CC	assaying the ability of the compound to modulate specific nucleic acid	
CC	CC	expression or polypeptide activity e.g. potassium channel, or kinase	
CC	CC	expression/activity. The method and compounds are useful for treating	
CC	CC	pain or painful disorders e.g. inflammatory pain, chronic pain,	
CC	CC	neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache	
CC	CC	pain and tissue pain. The present sequence encodes a human protein	
CC	CC	associated with pain.	
XX	XX		
SQ	SQ	Sequence 6574 BP; 1877 A; 1611 C; 1776 G; 1310 T; 0 U; 0 Other;	
Query Match 92.3%; Score 1397.8; DB 10; Length 6574;			
Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1402; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
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Db	13	GGGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCTTTGGATGCTGCTGCTGAA	72
Qy	61	CCCATTCGCCAACCGGGCTCCAGGCTGAATCTGTCTTCCAGGGGAACACACCTTTATG	120
Db	73	CCCATTCGCCAGCGGGCTCCAGGCTGAATCTGTCTTCCAGGGGAACACACCTTTATG	132
Qy	121	ACTCAACAGCAGATGTCCTCTTTTCCGAGAGGGATATAGATGCCCTTTTGTTC	180
Db	133	ACTCAACAGCAGATGTCCTCTTTTCCGAGAGGGATATAGATGCCCTTTTGTTC	192





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 02:03:14 ; Search time 6341 Seconds  
(without alignments)  
11298.517 Million cell updates/sec

Title: US-10-724-594-1

Perfect score: 1515

Sequence: 1 gggagagatgtgaagttaa.....tcgagccgctgatccgta 1515

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1515	100.0	1515	6	AR253937 Sequence
2	1515	100.0	1515	6	AR453415 Sequence
3	1510.2	99.7	2056	6	AX642956 Sequence
4	1305.8	99.4	1785	6	AX671044 Sequence
5	1481.8	97.8	1485	6	AX671037 Sequence
6	1404.2	92.7	6298	6	AX504254 Sequence
7	1404.2	92.7	8576	9	AY257469 Homo sapi
8	1398.2	92.4	1799	9	AY209000 Homo sapi
9	1398.2	92.3	5877	6	AX574427 Sequence
10	1398.2	92.3	6156	6	AX671112 Sequence
11	1398.2	92.3	6165	6	AX574425 Sequence
12	1398.2	92.3	6165	6	AX671105 Sequence
13	1398.2	92.3	8603	6	AX671108 Sequence
14	1397.8	92.3	6574	6	AX429512 Sequence
15	1391.8	91.9	6159	6	AX429514 Sequence
16	1382	91.2	6159	6	AX166510 Sequence
17	1375.8	90.8	6189	6	AX503780 Sequence
18	1375.8	90.8	6201	6	AX503778 Sequence
19	1158	76.4	2380	6	AX671042 Sequence

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21	1090	71.9	6954	10	AF086824	AF086824 Mus muscu
22	1082	71.4	1386	10	AF070065	AF070065 Rattus no
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24	760.8	50.2	1133	6	AR475453	AR475453 Sequence
25	578.8	38.2	2896	6	CQ498283	CQ498283 Sequence
26	455	30.2	5920	6	CQ723254	CQ723254 Sequence
27	441.8	29.2	446	6	CQ483947	CQ483947 Sequence
28	434.4	28.7	485	6	CQ513776	CQ513776 Sequence
29	288.8	19.1	2284	9	AX123136	AX123136 Homo sapi
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32	247.2	16.3	3835	6	AX817259	AX817259 Sequence
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34	246.8	16.3	1530	6	AX504235	AX504235 Sequence
35	246.8	16.3	4680	9	AY648038	AY648038 Homo sapi
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38	246.8	16.3	5373	6	AX746189	AX746189 Sequence
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40	240	15.8	6335	6	AX827351	AX827351 Sequence
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42	236.8	15.6	4917	9	AY166586	AY166586 Homo sapi
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44	234.6	15.5	4917	9	HSAS18976	AJ518976 Homo sapi
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## ALIGNMENTS

RESULT 1	AR253937	Sequence 1	from patent US 6479269.	1515 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	AR253937	Sequence 1	from patent US 6479269.	1515 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 1	from patent US 6479269.	1515 bp	DNA	linear	PAT 20-DEC-2002	
ACCESSION	AR253937	Sequence 1	from patent US 6479269.	1515 bp	DNA	linear	PAT 20-DEC-2002
VERSION	AR253937.1	GI:27302420					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1515)						
AUTHORS	Webster, M., Yan, C., Di Francesco, V. and Beasley, E. M.						
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof						
JOURNAL	Patent: US 6479269-A 1 12-NOV-2002;						
FEATURES	Location/Qualifiers						
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QY	61	CCCAATCCCAACCGGGCTCCAGGCTAAATCTGTTCTTCCAGGGGAAACCAACCCCTTTATG	120		
Db	61	CCCAATCCCAACCGGGCTCCAGGCTAAATCTGTTCTTCCAGGGGAAACCAACCCCTTTATG	120		
QY	121	ACTCAACAGCAGATGCTCTCTTTCCCGAGAGGGATATTAGATGCTCTTTGTTCTC	180		
Db	121	ACTCAACAGCAGATGCTCTCTTTCCCGAGAGGGATATTAGATGCTCTTTGTTCTC	180		
QY	181	TTTGAAAGTGCAGTGCAGCTGCTCTGATGAAGATTAAAGCAGTGCAGCAACTTTGTCGG	240		
Db	181	TTTGAAAGTGCAGTGCAGCTGCTCTGATGAAGATTAAAGCAGTGCAGCAACTTTGTCGG	240		
QY	241	AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGCCTTCGGCAAGGACTTCGAA	300		







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 QY 847 GGCCTGAGCTGACTGGTGTGCTAGTGGCGGTGATTCCTATGAGATGATTTATGGAGA 906  
 Db 841 GGCCTGAGCTGACTGGTGTGCTAGTGGCGGTGATTCCTATGAGATGATTTATGGAGA 900  
 QY 907 TCCCTCTTCGAGAGGAACTCTGCGCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 966  
 Db 901 TCCCTCTTCGAGAGGAACTCTGCGCAGAACCTTCAATAACATTAATGAATTTCCAGCGG 960  
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 Db 961 TTTTGAATTTCCAGATGACCCCAAGTAGAGAGTGAATTTCTGATCTGAATCAAAAGC 1020  
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 QY 1087 TCTAAATGACTGGAACAACTTCGTAACCTCTCTCCCTCCCTTCGTTCCACCCCTCAAG 1146  
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 Db 1141 TCTGACGACGACCTCCAACTTTGATGAACCCAGAGAGAAATTCGTTGCTCTCT 1200  
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RESULT 5  
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 LOCUS 1485 bp DNA linear PAT 27-MAR-2003  
 DEFINITION Sequence 1 from Patent WO03004629.  
 ACCESSION AX671037  
 VERSION AX671037.1 GI:29329507  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Zhu,Z  
 TITLE Regulation of human citron rho/rac-interacting kinase-short kinase  
 JOURNAL Patent: WO 03004629-A 1 16-JAN-2003;  
 Bayer Aktiengesellschaft (DE)  
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## RESULT 7

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LOCUS Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete cds.  
DEFINITION AY257469  
ACCESSION AY257469.1 GI:30088969  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 8576)  
Huang, C.Q., Wu, S.L., Shan, Y.X., Liu, S. and Xiao, P.J.  
Direct Submission  
Submitted (18-MAR-2003) Department of Biochemistry and Molecular Biology, Basic Medicine, Suzhou University, Renming Road 48, Suzhou, Jiangsu 215007, China  
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## FEATURES

## source

## gene

## CDS

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## ORIGIN

Query Match 92.7%; Score 1404.2; DB 9; Length 8576;  
Best Local Similarity 99.8%; Pred. No. 0;  
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 VERSION AX574427.1 GI:27551752  
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 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 Yu, X., Miranda, M. and Friddle, C.J.  
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ACCESSION      AX574425
VERSION        AX574425.1 GI:27551751
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REFERENCE      1
AUTHORS       Yu, X., Miranda, M. and Fiddle, C.J.
TITLE         Human kinases and polynucleotides encoding the same
JOURNAL       Patent: WO 02059325-A 1 01-AUG-2002;
              Lexicon Genetics Incorporated (US)
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REFERENCE      1
AUTHORS       Zhu, Z.
TITLE         Regulation of human citron rho/rac-interacting kinase
JOURNAL       Patent: WO 03004523-A 1 16-JAN-2003;
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VERSION AX429512.1 GI:21540791  
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REFERENCE  
1 Kapeller-Libermann, R.  
AUTHORS 13245, a novel human myotonic dystrophy type protein kinase and  
TITLE uses therefor  
JOURNAL Patent: WO 0234896-A 1 02-MAY-2002;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6	2157.5	82.9	448	Q88527	Q88527 rattus norv
7	929	35.7	717	Q8AXM0	Q8axm0 xenopus lae
8	929	35.7	1551	Q6DR37	Q6dr37 homo sapien
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38	847	32.6	631	1 DMK_MOUSE	P54265 mus musculus
39	837.5	32.2	1379	1 ROC2_RAT	Q62868 rattus norv
40	822.5	31.6	639	1 DMK_HUMAN	Q09013 homo sapien
41	809	31.1	1390	2 Q9U779	Q9u779 drosophila
42	809	31.1	1390	2 Q9VXE3	Q9vxe3 drosophila
43	809	31.1	1390	2 Q961D4	Q961d4 drosophila
44	778.5	29.9	865	2 Q98SN6	Q98sn6 gallus gall
45	763.5	29.3	289	2 O00565	O00565 homo sapien

## ALIGNMENTS

### RESULT 1

ID	Q86UQ9	PRELIMINARY;	PRT; 2027 AA.
AC	Q86UQ9;		
DT	01-JUN-2003 (Tremblrel. 24, Created)		
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	Rho/rac-interacting citron kinase.		
GN	Name=CIT;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Huang C.Q., Wu S.L., Shan Y.X., Liu S., Xiao P.J.;		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.		
DR	HSSP; AY257469; AAPI3528.1; -		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0005524; P:ATP binding; IEA.		
DR	GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0005089; P:small GTPase regulatory/interacting protein. . .; IEA.		
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.		
DR	GO; GO:0006469; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR001180; Citron.		
DR	InterPro; IPR005479; Cphp synth_L_D2.		
DR	InterPro; IPR002219; DAG_Ps-bind_.		
DR	InterPro; IPR011009; Kinase_like.		
DR	InterPro; IPR001849; PH.		
DR	InterPro; IPR000961; Pkinase_C.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR000861; REM_repeat.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	InterPro; IPR008271; Ser_thr_pkin_AS.		
DR	Pfam; PF00130; Cl_1; 1.		
DR	Pfam; PF00780; CNH; 1.		
DR	Pfam; PF00169; PH; 1.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	Pfam; PF00433; Pkinase_C; 1.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	SMART; SM00109; Cl; 1.		
DR	SMART; SM00036; CNH; 1.		
DR	SMART; SM00233; PH; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	SMART; SM00133; S_TK_X; 1.		
DR	PROSITE; PS00867; CFSASE_2; UNKNOWN_1.		
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.		
DR	PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.		
DR	PROSITE; PS50003; PH_DOMAIN_1.		
DR	PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS50108; PROTEIN_KINASE_ST; 1.		

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 2027 AA; 231429 MW; 681D8C3F661F357B CRC64;

Query Match 93.8%; Score 2440; DB 2; Length 2027;  
Best Local Similarity 99.6%; Pred. No. 2.1e-154;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLKFYGARNPDLGAAAEPTIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60
DB 1 MLKFYGARNPDLGAAAEPTIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
DB 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
QY 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVD 240
DB 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVD 240
QY 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMYYGR 300
DB 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMYYGR 300
QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFDLQSLGCGKERLKFGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFDLQSLGCGKERLKFGLCCHPFF 360
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420
DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKM 468

```

## RESULT 2

```

Q6XUH8 PRELIMINARY; PRT; 482 AA.
ID AC Q6XUH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Citron Rho-interacting kinase short form.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Wu Q.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- Similarity: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY209000; AAF43922.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002250; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR SMART; SM00133; S_TKc_1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

```

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 482 AA; 54353 MW; 4F02AF6A32C73BAE CRC64;

Query Match 93.2%; Score 2425; DB 2; Length 482;  
Best Local Similarity 98.9%; Pred. No. 3.4e-154;  
Matches 463; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MLKFYGARNPDLGAAAEPTIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60
DB 1 MLKFYGARNPDLGAAAEPTIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
QY 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
DB 121 DIYAMKMKKALLAQEQVFFBEERNILSRSTSPWIPOLQYAFQDKNHLVLMYEQPGG 180
QY 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVD 240
DB 181 DLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGHIKLVD 240
QY 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMYYGR 300
DB 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVIAEMYYGR 300
QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFDLQSLGCGKERLKFGLCCHPFF 360
DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFDLQSLGCGKERLKFGLCCHPFF 360
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420
DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSSPQQLSPGSGEELPFVGF 420
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKV 468
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKLLIKSKELQSDQKCHKM 468

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## RESULT 3

```

AAP43922 PRELIMINARY; PRT; 482 AA.
ID AAP43922;
AC AAP43922;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Citron Rho-interacting kinase short form.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Wu Q.;
RL "Cloning and characterizing a novel human CR1K-SK gene.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY209000; AAP43922.1; -.
KW Kinase.
SQ SEQUENCE 482 AA; 54353 MW; 4F02AF6A32C73BAE CRC64;

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Query Match 93.2%; Score 2425; DB 2; Length 482;  
Best Local Similarity 98.9%; Pred. No. 3.4e-154;  
Matches 463; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MLKFYGARNPDLGAAAEPTIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60
DB 1 MLKFYGARNPDLGAAAEPTIANRASRLNLFQGGKPPFMTQQQMSPLSRGILDALFVLPE 60
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120
DB 61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVRKATG 120

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QY 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 DB 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDIKPNILVDRTHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDIKPNILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNMKNVNAKLPIGTPDYMAPEVLTVMGDGKGYGLDCDMSVGVIAIYMIYGR 300  
 DB 241 GSAAKNSNMKNVNAKLPIGTPDYMAPEVLTVMGDGKGYGLDCDMSVGVIAIYMIYGR 300  
 QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 QY 361 SKIDWNINRNSPPFPVPTLKSDDDTNSFDEPEKNSVSSPCQLSPSGFSGEELPFVGF 420  
 DB 361 SKIDWNINRNSPPFPVPTLKSDDDTNSFDEPEKNSVSSPCQLSPSGFSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKM 468

## RESULT 4

O88937 PRELIMINARY; PRT; 494 AA.  
 AC O88937;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Rho/rac-interacting citron kinase short isoform.  
 GN Name-Cit; Synonyms=Crik-sk;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99009084; PubMed=9792683;  
 RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,  
 RA Dotto G.P.;  
 RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase  
 RT encompassing the Rho-Rac-binding protein Citron.";  
 RL J. Biol. Chem. 273:29706-29711(1998).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF086823; AAC72822.1; -;  
 DR HSP; F31751; IGZK.  
 DR MGD; MGII:105313; Cit.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase-like.  
 DR InterPro; IPR000961; Kinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00069; Pkinase\_I.  
 DR Pfam; PF00433; Pkinase\_C1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 494 AA; 55742 MW; 2C60D2294B28A185 CRC64;

Query Match 97.3%; Score 2271.5; DB 2; Length 494;  
 Best Local Similarity 97.3%; Pred. No. 6.8e-144;

Matches 432; Conservative 27; Mismatches 35; Indels 1; Gaps 1;  
 QY 1 MLKFKYGARNPLDAGAAPIANRASRLNLPFGKPPFTQOQMSPLSREGILDALFVLFE 60  
 DB 1 MLKFKYGARNPLDAGAAPIANRASRLNLPFGKPPFTQOQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQALMKIKHNSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVVRKATG 120  
 DB 61 ECSQALMKIKHNSNFVKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVVRKATG 120  
 QY 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 DB 121 DIYAMKMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 QY 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDIKPNILVDRTHIKLVDF 240  
 DB 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGYVHRDIKPNILVDRTHIKLVDF 240  
 QY 241 GSAAKNSNMKNVNAKLPIGTPDYMAPEVLTVMGDGKGYGLDCDMSVGVIAIYMIYGR 300  
 DB 241 GSAAKNSNMKNVNAKLPIGTPDYMAPEVLTVMGDGKGYGLDCDMSVGVIAIYMIYGR 300  
 QY 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 DB 301 SPFAEGTSARTFNINMNFQFLKPPDDPKVSSDFLDLIQSLCGQERLKFEGLCCHPFF 360  
 QY 361 SKIDWNINRNSPPFPVPTLKSDDDTNSFDEPEKNSVSSPCQLSPSGFSGEELPFVGF 420  
 DB 361 SKIDWNINRNSPPFPVPTLKSDDDTNSFDEPEKNSVSSPCQLSPSGFSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVIFISAAGLPCSR 480  
 DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKVIFISAAGLPCSR 480  
 QY 481 ILPSVYAKGSARGC 495  
 DB 480 ILQSIYAEAGSAGGHC 494  
 RESULT 5  
 O88938 PRELIMINARY; PRT; 2055 AA.  
 AC O88938;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Rho/rac-interacting citron kinase.  
 GN Name-Cit; Synonyms=Crik;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=99009084; PubMed=9792683;  
 RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,  
 RA Dotto G.P.;  
 RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase  
 RT encompassing the Rho-Rac-binding protein Citron.";  
 RL J. Biol. Chem. 273:29706-29711(1998).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF086824; AAC72823.1; -;  
 DR HSP; F31751; IGZK.  
 DR MGD; MGII:105313; Cit.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein...; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001180; Citron.  
 DR InterPro; IPR005479; Cphp\_synth\_L\_D2.



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RESULT 7
Q8AVM0
ID Q8AVM0 PRELIMINARY; PRT; 717 AA.
AC Q8AVM0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cdc42bpb protein (Fragment).
GN Name=Cdc42bpb;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson D.K., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bonfield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC 1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC041741; AA041741.1; -.
DR HSP; P31751; IGZK.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 717
SQ SEQUENCE 717 AA; 83371 MW; 2D295D4A8A5B733A CRC64;

Query Match 35.7%; Score 929; DB 2; Length 717;
Best Local Similarity 41.7%; Pred. NO. 9.7e-54;
Matches 196; Conservative 84; Mismatches 148; Indels 42; Gaps 10;

QY 23 RASRLNLPFGKPPFTMQQMSPLSGREGILDALFVLFECSQPALMKIKHVNFEV---RK 79
Db 6 RLKRLQLLDGP-----QRNEAAVSUTLDDVLLCLTCTSTLRDKYSEFEWAKP 61
QY 80 YSTIAELQELQPSAKDPFVRLVCGCHFAEYVVRKATGDIYAMKVMKKALLAQEQV 139
Db 62 F*DL---LKGMLHRDDFIIKVGCGAFGEVAVVRLKSTERYAMKILNKWEMLKRAET 118
QY 140 SPFEERNILSRSTSPWIPOLQYAFQDKNHLVMEYQPGGDLISLNRYEDLDENLIQ 199
Db 119 ACFREERNVLVNGDQOWITTLHYAFQDENLYLVMDYVVGDLTLTLKSFEDLPEDMSR 178
QY 200 FYLAELILAVSHVLMGVYVRDIKPNILVDRTGHIKLVDFGSAAKMNSNMVNAKLPTG 259
Db 179 FYLAEMVLAIHSIHQLHYVVRDIKPDNILLDMNGHRLADFGCLKMKNDGTVQSSVAVG 238
QY 260 TPDYVAPEVLTVNGDGKTYGLDCDWMSVGVIAMETIYGRSPFAEGTSARTFNMMNPQ 319
Db 239 TPDYISPEILOAME-DGMGKYGFECDMWSLGVCMVEMLYGETFPFYAESLIVETYGIMNHE 297
QY 320 RELKFPDD-PKYSDFDLDIQSLCGOKERLKFEG---CCHPFFSKIDMNNRNSPPPF 375
Db 298 ERFQPPSHIGDVSESAKLIQLICSRERRIQNGIDDFKAHPFEGIDWDNRINLEAPY 357
QY 376 VPTLKSDDDTSNFDPPE---KNSVSSSPCQLSPSGSGEELPFVGFYSYK----- 423
Db 358 IPDVSSPSPSTNFDVDDDDILRNPVIPS---THSGFGSGFHLPPFVGFTYTDSCFSDRGS 414
QY 424 ----ALGILGRSESVSLGSDSPAKTSMEKKL-----LIKSELODS 461
Db 415 LKDTIHANAVTKDEDVQRLQSLQVDAYERRIRLEQEKLELNRLQES 464

RESULT 8
Q6DT37
ID Q6DT37 PRELIMINARY; PRT; 1551 AA.
AC Q6DT37;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Myotonic dystrophy kinase-related CDC42-binding kinase gamma.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ng Y., Tan I., Lim L., Leung T.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY648038; AAT67172.1; -.
KW Kinase.
SQ SEQUENCE 1551 AA; 172517 MW; 6B2DCED7BFE57B1E CRC64;

Query Match 35.7%; Score 929; DB 2; Length 1551;
Best Local Similarity 43.8%; Pred. NO. 2.6e-53;
Matches 184; Conservative 83; Mismatches 125; Indels 28; Gaps 7;

QY 49 EGILDALFVLFECSQPALMKIKHVNVRKYSTIAELQELQPSAKDPFVRLVCGCHP 108
Db 23 DGLDLLLALHHELSGSLRRERSVAQFLSWASPFVSKVKELRLQRDDDFELKVGRAF 82
QY 109 AEQVVVRKATGDIYAMKVMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKN 168
Db 83 GEVTVVRQDGTGQIFAMQMLHKEMLKAEATACFREEDVLVKGDSRWVTLHYAFQDEE 142

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169 HLYVMVEYOPGGDLILNRYEDQDENLITQFYLAELIAVSHVLMGYVHRDKPENIL 228  
 143 YLYLWYDYAGGDLILNRYEDQDENLITQFYLAELIAVSHVLMGYVHRDKPENIL 202  
 229 VRTGHIKLVDFGSAKMSKNNKAKLIGIPDPYMAPEVLTVMGDKGTGVLGDCDWS 288  
 203 LDVNGHRLADFSCURLNTNGVDSVAVGTPDYISPEILOAME-EGKGHYGPOCDWWS 261  
 289 VGVIAEMLYGRSPFAEGTSARTFNINMFQRFLEKPPDD-PKVSSDFLLIOLSLCGQKE 347  
 262 LGVCAYELLPGEFFVARSILVYGYKIMHDEHQLQFPDPVDPVPSAQDLIQLLCRQEE 321  
 348 RLKFEGL---CCHPFSKIDWNIRNSPPFPVFTLSDDDTNSFDPKNSWSSPCOL 404  
 322 RLGRGLDDPRNHPFFEGVDWRERLSTAPYIPELRGMPTDNFDDDD---TLNHPGTL 378  
 405 SP---SGFSEELPFVGFYSXKALGILGRSESVSGLDSPAKTS-----SMEKKLIKSKKE 457  
 379 PPSHGAFSGHLPFFVGFYIT-----SGSHFSESSENAALERKLCLEGE 425

RESULT 9  
 Q9VTY8  
 ID Q9VTY8 PRELIMINARY; PRT; 1854 AA.  
 AC Q9VTY8  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE CG10522-PA.  
 GN ORFNames=CG10522;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananthan S., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Bland M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Flesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Moberly C.C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M.D., Skupski M.P., Smith I.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 "The genome sequence of Drosophila melanogaster";  
 Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 melanogaster euchromatic genome sequence";  
 Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 "The transposable elements of the Drosophila melanogaster euchromatin:  
 a genome perspective";  
 Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 "Annotation of the Drosophila melanogaster euchromatic genome: a  
 systematic review";  
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX FLYBASE;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RG FLYBASE;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AE003541; AAF49907.2; --  
 DR HSRF; P31751; IGZK.  
 DR InAct; Q9VTY8; --  
 DR FlyBase; FBgn0036295; CG10522.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein.; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPRO01180; Citron.  
 DR InterPro; IPRO02219; DAG\_PE-bind.  
 DR InterPro; IPRO02219; DAG\_PE-bind.  
 DR InterPro; IPRO01009; Kinase like.  
 DR InterPro; IPRO00961; Kinase C.  
 DR InterPro; IPRO00719; Prot\_kinase.  
 DR InterPro; IPRO00290; Ser\_thr\_kinase.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00069; PKinase; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00133; S\_TKc; 1.  
 DR PROSITE; PS00081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SEQUENCE 1854 AA; 211323 MW; 93B5B69FE63DEE1D CRC64;



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Query Match 35.4%; Score 922; DB 2; Length 1854;
Best Local Similarity 40.1%; Pred. No. 9.5e-53;
Matches 194; Conservative 99; Mismatches 129; Indels 62; Gaps 9;

QY 18 BPIANRSLNLFQGGK-----PFMTQQQMSPLS-----REG 50
Db 6 EPISVTRALNLIIGKAGVCAKPGASGSGIPASTRRSIVPVSTTSAABAICREG 65
QY 51 ILDALFVLFECSQPALMK-IKHSNFRVKYSYDTIAELQELQPSAKDFEVSRLVCGHFA 109
Db 66 LLDAFCLLVNECDKTLKRDENIAEFVKNRPIIEETRKLRVADDELIKTLGQGYFG 125
QY 110 EVQVVRKATGDIYAMKWKALLAQOVSFFBEERNILSRSTSPWIPQLQYAFQKNH 169
Db 126 NVHLVVERQTDIYAMKIKKSVVTSQ-----VKEEDIMGRSEWLNQLQYAFQNDN 181
QY 170 LYLVMYQPGGDLNLNRYEDQDENLIQVLAELIYAVSHVLMGVVHRDIKPNILV 229
Db 182 LYLVMYVPGGDLNLSERH-GPDEDLARYFLAELTVALTLEMGVVHRDIKPNILI 240
QY 230 DRTGHIKLVDFGSAKNSNKNVNAKPIGTPDYMAPEVLVWNGD--GKTYGLDCDW 287
Db 241 DRFGHIKLADPENAALDRDGHVLSLSPVGTVDYIAPELLQTIYSTYKLSKSMHDVSCDY 300
QY 288 SVGLVAYEMVYGRSPEAGTSARTFNIM-----NQRFLKFPDDPKVSDFDLIQSL 341
Db 301 SMGIGYELICETTFHEDNVHTYKLSHCESSHLKELISFPFADLVKSVYVNRNLIES 360
QY 342 LCGOKERLKFGLCHPFFSFKIDWNIRNSPPVPVTLKSDDDTSNFD-----PEKN 394
Db 361 VTNPSKRLSYERIKNHPFSPISPGSIRSQVPIPIVRSDDDDTSNFDGIRHKTRREG 420
QY 395 SWVSSPQLSPFSGSELPFGVFSKALGILGRSESVVGLDSPAKTSSMEKLLIK 454
Db 421 VAKSLTNMKSNDFSGKDLFFIGYSFVH-----MEKSAISATTDKLEQX 466
QY 455 SKEL 458
Db 467 LKEL 470

RESULT 10
O01583 PRELIMINARY; PRT; 1592 AA.
AC O01583;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein K08B12.5.
GN ORFNames=K08B12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Becker M., Wohldmann P.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

[4]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; U97001; AAB52260.3; -.
PIR; T25808; T25808.
HSP; P31751; IGZK.
DR WormPep; K08B12.5; CE30818.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000095; PKBox/Rhobndng.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50108; CRIB; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
SQ Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1592 AA; 180743 MW; P909FA8F5C9876C CRC64;

Query Match 34.5%; Score 897.5; DB 2; Length 1592;
Best Local Similarity 40.5%; Pred. No. 3.4e-51;
Matches 178; Conservative 91; Mismatches 150; Indels 21; Gaps 8;

QY 28 NLFFGKPPFMTQQQMSPLSREGILDALFVLFECSQPALMKIKHSNFRVKYSYDTIAEL 87
Db 19 NIYMDG-----PSKKPEALSPETLIDSLICLYDECCNSTLRKEKICIAFFVESKTVISKA 73
QY 88 QELQPSAKDFEVSRLVCGHFAEVQVREKATGIYAMKWKALLAQOVSFFBEERN 147
Db 74 KKLRLSRDDFEVLKVIKGAGFGEVAVVMRGVGIYAMKILNKMVWKRAETACFEERD 133
QY 148 ILSRSTSPWIPQLQYAFQDKNHLVLMYVQPGDLSLLNRYEDQDENLIQVLAELIL 207
Db 134 VLIVYGDNRWITNLHVAFODEKNLIFVMDYIYGGDMLTLLSKFVDHI PSMKAFYIAENVL 193
QY 208 AVHSVHLMGYVHRDIKPNILVDRTHIKLVDFGSAKNSNKNVNAKPIGTPDYMAPE 267
Db 194 AIDSLRLGYVHRDVKPDNVLDMQGHIRLADFGSLRILADGVSASVAVVGTEDYISPE 253
QY 266 VLTVMVNGDKGTGYGLDCDWWSVGLVAYEMVYGRSPEAGTSARTFNIMNFORLKPDD 327
Db 254 ILRAME-DGRYRKGECWWSLGMVEMLYGTFFYSERLVDYTGKIMSDMLDFPDD 312
QY 328 P---KVSSDFLDLIQSLCGOKERLKFGLC---CHPFFSKIDWNIRNSPPVPVTLKS 381
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Db      313 EIDWVWSEAKOLIRQLICSSDVRFGRLGLSDFLQHPFFEGIDWNTIRDSNPPYVPEVSS 372
QY      382 DDDTSNFDPEKNSWSSSPC--QLSP---SGFSGEELPFVGFYSYKALGILGRSESV 435
Db      373 PEDTSNFDVDCBD--DFTPCLOETQPPVLAFTGNHLPFVGFSTHG--SLLSDARSUT 429
QY      436 SGLDSPAKTSSMEKLLIKS 455
Db      430 DEIRATAQRCQGAELMEKS 449

RESULT 11
Q86X28 PRELIMINARY; PRT; 492 AA.
ID AC Q86X28;
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC048261; AAH48261.1; -.
DR HSSP; P31751; 1GZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 492
SQ SEQUENCE 492 AA; 56805 MW; 5F9FBD9CC1D2A3FC CRC64;

Query Match 34.5%; Score 896.5; DB 2; Length 492;
Best Local Similarity 42.1%; Pred. No. 9.1e-52;
Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;

QY 44 SPASREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVSUV 103
Db 23 SALSVEITLLDLVCLYTECSHLSALRDKYVAEFLWAKPFTQLVKEMQLHREDFEIKVI 82
QY 104 GCGHFAEVQVREKATGDIYAMKVMKKALLAQBQVSVFFEEERNILSRSTSPWIPOLQYA 163
Db 83 GRGAFGEVAVVMKQNTERRIYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYA 142
QY 164 FQDKNHLVLYMEYQPGGDLISLLNRYEDQDENLIQIYLAELILAVSHVLMGYVHRDIK 223
Db 143 FQDENHLVLYMVDYVVGDDLTLISKFEDKLPEDMARFYIGEMVLAIIDSIHQLHYVHRDIK 202
QY 224 PENILVTRTHIKLVDFGSAKNSNMVNAKLPIGTPDYMAPEVLTVMGDGGTYGLD 283
Db 203 PDNVLLDVNGHIRLADFGSCLKMDNDGTVOSSVAVGPDYIISFELQAE--DMGKXGPE 261
QY 284 CDWMSVGVIAYEMTYGRSPFAEGTSARTFNINMNFQRLKFPDD--PKVSDDFLDLQSL 342
Db 262 CDWNSLGVCMYEMLYGETPFVAESLVETGYKIMNHEERFQFPSSHVDVSEAKDLIQLRI 321
QY 343 CGQKERLKFEGL---CHPFFSKIDMNNIRNSPPFPVPTLKSDDDTSNFDPEPE---KNSW 396
Db 322 CSRERRLQNGIEDFKHAFPEGLNWNIRNLEAPIYDVSSPSDTSNFDVDDVLNRTE 381
QY 397 VSSSPCQLSP---SGFSGEELPFVGFYSYKALGILGRSESVSGLDSPAKTSSMEKLLI 453
Db 392 I-----LPPGSHTFPSGLHLPFGIFFT-----TESCFs--DRGSLKSIQSNLT 425
QY 454 KSKELQDSQDKCHKVFISA 472
Db 426 KDEVDVQ--RDLEHSLQMEA 442

RESULT 12
Q86TJ1 PRELIMINARY; PRT; 933 AA.
ID AC Q86TJ1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CDC42BPB protein (Fragment).
GN Name=CDC42BPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC048261; AAH48261.1; -.
DR HSSP; P31751; 1GZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

```

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RA Strausberg R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; BC047871; AAH47871.1; --  
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 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000961; Kinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 FT NON TER 933  
 SQ SEQUENCE 933 AA; 108543 MW; 38E7179C3253F521 CRC64;  
 Query Match 34.5%; Score 896.5; DB 2; Length 933;  
 Best Local Similarity 42.1%; Pred. No. 2e-51;  
 Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;  
 QY 44 SPLSGREGILDALFVLEECQSPALMKIKHVSFVKYSDTIAELQELQPSAKDFEVSRLV 103  
 DB 23 SALSVEILLDLVLCYTECHSALRRDKYVAEFLWAKPTQLVKEMQLHREDFEIKVI 82  
 QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163  
 DB 83 GRGAFGEVAVVVKMNTIRIYAMKILNKWMLKRAETACFREEDVLVNGDCQWITALHYA 142  
 QY 164 FQDKNHLIYLMVEYQPGDLSLLNRYEDQDENLIQFYLAELILAVHSVHLMGVHRDIK 223  
 DB 143 FQDENHLYLVMDYVVGDLTLTLKSKFEDKLPEDMARFYIGEMVLAIIDSIIHQLHYVHRDIK 202  
 QY 224 PENILVDRTHGHIKLVDFGSAKSNKRNKVNAKLPIGTDPYMAPEVLTVNMGDKGYGLD 283  
 DB 203 PDNVLLDVNGHIRLADFGSLKWNDDGTVOSSVAVGTFDVISPEILQAME-DNGKYGPE 261  
 QY 284 CDWWSGVVIAYEMIYGRSPFAEGTSARTFNNINMFORLFPDD-PRVSSDFDLIQLSL 342  
 DB 262 CDWWSLGVCMYEMLYGETPYAESLVETYGKIMHEERFQPSHVTDVSEAKDLIQLRI 321  
 QY 343 CGQKERLKFGL---CCHPFESKIDWNINSPFPVPTLKSDDDTSNDEPE---KSNW 396  
 DB 322 CSHERRLGQNGIEDFKKHAFEGGLNMENTIRNLAPYIPDVSPSDTSNFDVDDVLRNTE 381  
 QY 397 VSSSPCOLSP---SGFSGEELPFVGFYSKALGILGRSESVWSGLDSPAKTSMKELLI 453  
 DB 382 I-----LPGSHGFGSLHLPFGTFTT-----TESCFs--DRGSLKSIQSNITLT 425  
 QY 454 KSKELQSQDKCHKVFISA 472  
 DB 426 KEDVQ--RDLEHSLQMEA 442  
 PRELIMINARY; PRT; 1711 AA.

AC Q9V532;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE CDC42-binding protein kinase beta.  
 GN Name=CDC42BPA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99216425; PubMed=10198171;  
 RA Moncrieff C.L., Bailey M.E., Morrison N., Johnson K.J.;  
 RT "Cloning and chromosomal localization of human Cdc42-binding protein  
 RT kinase beta.";  
 RL Genomics 57:297-300(1999).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF128625; AAD37506.1; --  
 DR HSSP; P31751; IGZK.  
 DR GO; GO:0005856; C:cytoskeleton; TAS.  
 DR GO; GO:0004672; F:protein kinase activity; TAS.  
 DR GO; GO:0007163; P:establishment and/or maintenance of cell po. .; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR001180; Citron.  
 DR InterPro; IPR002219; DAG PE-bind.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000095; PAKbox/RhoBindg.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00130; Cl\_1; 1.  
 DR Pfam; PF00780; CNH; 1.  
 DR Pfam; PF00786; PBD; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR PRINTS; PR00008; DAGPEDOMAIN.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR SMART; SM00109; Cl; 1.  
 DR SMART; SM00036; CNH; 1.  
 DR SMART; SM00285; PBD; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00220; S\_TK\_X; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR PROSITE; PS00108; CRTB; 1.  
 DR PROSITE; PS00479; DAG PE BIND DOM 1; 1.  
 DR PROSITE; PS00081; DAG PE BIND DOM 2; 1.  
 DR PROSITE; PS00003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1711 AA; 194356 MW; 3A3731D40A363497 CRC64;  
 Query Match 34.5%; Score 896.5; DB 2; Length 1711;  
 Best Local Similarity 42.1%; Pred. No. 4.4e-51;  
 Matches 185; Conservative 85; Mismatches 140; Indels 29; Gaps 9;  
 QY 44 SPLSGREGILDALFVLEECQSPALMKIKHVSFVKYSDTIAELQELQPSAKDFEVSRLV 103  
 DB 23 SALSVEILLDLVLCYTECHSALRRDKYVAEFLWAKPTQLVKEMQLHREDFEIKVI 82  
 QY 104 GCGHFAEVQVVRKATGDIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163  
 DB 83 GRGAFGEVAVVVKMNTIRIYAMKILNKWMLKRAETACFREEDVLVNGDCQWITALHYA 142  
 QY 164 FQDKNHLIYLMVEYQPGDLSLLNRYEDQDENLIQFYLAELILAVHSVHLMGVHRDIK 223  
 DB 143 FQDENHLYLVMDYVVGDLTLTLKSKFEDKLPEDMARFYIGEMVLAIIDSIIHQLHYVHRDIK 202

RESULT 13  
 Q9V532  
 ID Q9V532



Search completed: November 8, 2004, 12:31:34  
Job time : 198 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 12:22:26 ; Search time 41 Seconds  
(without alignments)  
1166.335 Million cell updates/sec

Title: US-10-724-594-2  
Perfect score: 2602  
Sequence: 1 MLKPKYGARNPLDAGAEPI.....CSRILPSVYAKSGARGCWL 497  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

- 1: Pir1.\*
- 2: Pir2.\*
- 3: Pir3.\*
- 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908.5	34.9	1548	2 T25808	hypothetical prote
2	891	34.2	1732	2 T14039	protein kinase (EC
3	883	33.9	1702	2 T14050	protein kinase (EC
4	876.5	33.7	1173	2 T25539	hypothetical prote
5	866.5	33.3	1354	2 S74244	serine/threonine-s
6	864.5	33.2	1354	2 S69211	serine/threonine-s
7	863	33.2	624	2 B49364	protein kinase (EC
8	860.5	33.1	1388	2 S70333	serine/threonine-s
9	853.5	32.8	1388	2 S74245	serine/threonine-s
10	847	32.6	557	2 S71829	serine/threonine-s
11	721	27.7	522	2 G86431	protein kinase T51
12	711	27.3	479	2 S42864	protein kinase (EC
13	704	27.1	756	2 S60966	probable protein k
14	701	26.9	526	2 S49077	protein kinase PKT
15	700	26.9	469	2 T41723	serine/threonine-s
16	697	26.8	596	2 F84589	probable protein k
17	693	26.6	549	2 A86170	hypothetical prote
18	687.5	26.4	474	2 I78396	myotonic dystrophy
19	685	26.3	441	2 I78393	myotonic dystrophy
20	685	26.3	516	2 I78394	myotonic dystrophy
21	682.5	26.2	1356	2 T16718	hypothetical prote
22	676.5	26.0	443	2 D71405	probable protein k
23	676.5	26.0	475	2 H81556	protein kinase [im
24	674.5	25.9	465	2 I38133	protein kinase (EC
25	665.5	25.6	500	2 S42867	protein kinase (EC
26	660.5	25.4	483	2 T05188	protein kinase F41
27	639	24.6	545	2 T01288	protein kinase F27
28	636.5	24.5	588	2 T47254	serine/threonine k
29	636.5	24.5	685	2 S70706	probable protein k

30	636	24.4	480	2 T47255	serine/threonine k
31	636	24.4	620	2 S22711	probable protein k
32	608	23.4	908	2 T25035	hypothetical prote
33	606.5	23.3	412	2 I78395	myotonic dystrophy
34	604	23.2	1099	2 A56155	tumor suppressor p
35	548	21.1	607	2 S62556	probable serine/th
36	536	20.6	624	2 T41341	probable serine-th
37	532.5	20.5	564	2 S59776	protein kinase DAF
38	522	20.1	572	2 S64387	protein kinase DBP
39	520.5	20.0	726	2 S22258	probable protein k
40	520	20.0	1092	2 H96509	protein F27F5.23 l
41	516	19.8	893	2 S63378	hypothetical prote
42	515	19.8	425	2 S41099	protein kinase (EC
43	510.5	19.6	646	2 T38171	probable serine/th
44	510	19.6	462	1 T17287	protein kinase (EC
45	509	19.6	569	2 T50414	probable prolifera

## ALIGNMENTS

### RESULT 1

T25808  
hypothetical protein K08B12.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Aug-2004  
C/Accession: T25808  
R:Becker, M.; Wohldmann, P.  
submitted to the EMBL Data Library, April 1997  
A:Description: The sequence of C. elegans cosmid K08B12.  
A:Reference number: Z20091  
A:Accession: T25808  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1548 <BEC>  
A:Cross-references: UNIPROT:O01583; EMBL:U97001; PIDN:AB52260.1; GSPDB:GN00023; CESP:K  
A:Experimental source: strain Bristol N2; clone K08B12  
C:Genetics:  
A:Gene: CESP:K08B12.5  
A:Map position: 5  
A:Introns: 39/1; 66/1; 156/3; 278/2; 391/3; 628/1; 1022/2; 1273/3; 1326/1; 1423/2; 1489/2; 1489/2;  
C:Superfamily: protein kinase homology  
F:956-1005/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match	34.9%	Score	908.5	DB	2	Length	1548
Best Local Similarity	40.6%	Pred. No.	2.3e-33				
Matches	178	Conservative	91	Mismatches	150	Indels	19
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Db	19	NIYMDG-----PSKAPALSFETLIDSLICYDCCNSTLRKCKCIAEFVESVKTVISKA	73				
Qy	88	CELOPSAKDFEVRSLVGGCHFAEQVVRKATGIYAMKVMKKALLAQEQVFPFEERN	147				
Db	74	KKLRSLRDDFEVLKVIKGAFGEVAVVMRGVGIYAMKILNKVMVKRAETACFREERD	133				
Qy	148	ILSRSTSWIQLQVAFQDKHLYLVMEYQGGDLLSLNRYEQDLNLFQVLAELIL	207				
Db	134	VLVYGDREWIINLHYAFQDEKNLYFVMDYIYGGDMLTLLSFVDHPIESMAKFIKAVL	193				
Qy	208	AVHSHLMGYVHRDIPKPNILVDRTGHIKLVDFGSAAMNSNMVNAKLPTGTPDYMAPE	267				
Db	194	AIDSLRLRGYVHRDVKPDVLLDQGHRLADFGSCLRLADGVSASVNAVGTEDYISPE	253				
Qy	268	VLTVNMGKGTGYGLDCDWSVGVIAYEMIVGRSPFAGTSAFTNNINFORLKFDD	327				
Db	254	ILRAME-DGRGRYKECDWSLIGICMVELYGTTPFYSERLVDTYVGKIMSHQDMLDFDD	312				
Qy	328	P---KVSSDFDLTQSLICGQKERLKPGLC---CHPFESKIDWNININSPPPVPTLKS	381				
Db	313	EIDWVVSSEAKDLRLQLICSSDVFGRNGLSDFQLHPFFEGIDWNTIRDSNPPVPEVSS	372				
Qy	382	DDTNSFDEPKNSWSSSPCQLSP----SGFSGEELPFVGFYSKALGILGRSESVSG	437				

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Db      373  PEDTSNFDVDCED--DETPCETOPPRVIAAFTGNHLPFGVFSYTHG-SILSDARSLTDE 429
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QY      438  LDSPAKTSMEKKLIKS 455
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      430  IRAIAORCOGDAELMEKS 447
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RESULT 2

Tl4039

protein kinase (BC 2.7.1.37), myotonic dystrophy-associated - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004

C:Accession: Tl4039

R:Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.

Mol. Cell. Biol. 18, 130-140, 1998

A:Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector

A:Reference number: Z17862; MUID:98078670; PMID:9418861

A:Accession: Tl4039

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1732 <LEU>

A:Cross-references: UNIPROT:O54874; EMBL:AF021935; NID:G2736150; PID:G2736151; PIDN:AAC0

C:Gene:cs

A:Gene: MRCK

C:Superfamily: protein kinase homology

C:Keywords: ATP; phosphotransferase

F:75-343/Domain: protein kinase homology <KIN>

F:1013-1062/Domain: protein kinase C zinc-binding repeat homology <KZN>

RESULT 3  
T14050  
protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2004  
C;Accession: T14050

R;leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.  
Mol. Cell. Biol. 18, 130-140, 1998  
A;Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector  
A;Reference number: Z17862; NUID:98078670; PMID:9418861  
A;Accession: T14050  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1702 <LEU>  
A;Cross-references: UNIPROT:O54875; EMBL:AF021936; PID:g2736152; NID:g2736153; PIDN:AAC0C  
A;Experimental source: brain

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RESULT 4
T25539
hypothetical protein C10H11.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25539
R:Dante, M.; Wamsley, P.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid C10H11.
A:Reference number: Z20047
A:Accession: T25539
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

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A;Residues: 1-1173 <DAN>  
A;Cross-references: UNIPROT:P92199; EMBL:U08811; PDB:1AAB2348.1; GSPDB:GN00019; CESP:CI0H11.9  
A;Experimental source: strain Bristol N2; clone CI0H11  
A;Genetics:  
A;Gene: CESP:CI0H11.9  
A;Map position: 1



A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 865/3; 891/3; 970/3; 1027/3; 1114/1  
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology

Query Match 33.7%; Score 876.5; DB 2; Length 1173;  
Best Local Similarity 40.9%; Pred. No. 4.7e-32;  
Matches 169; Conservative 88; Mismatches 142; Indels 13; Gaps 6;

QY 44 SPLSRGILDALFVLFECSQPALMKIKHVSFVRKYSQTIABQLQPSAKDFEVRSLV 103  
DB 15 SPINISLLDTITALVNDCKIPVLMRMKSVDFNISRYERWESLAALRMKAADFRLQKVI 74

QY 104 GCCHFAEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSWIPOLQYA 163  
DB 75 GRGAFGEVQLVRHKSTRKYAMKLLSKFEMIKRSASFFWEERDIFAFANSPWVQLFYA 134

QY 164 FQDKNHLVLMVEYQPGDLSILNRYEDQDENLIQFYLAELILAVHSLMGVYHRDIK 223  
DB 135 FQDPRHLYMVEYMPGGDLVNLMSYE--VSEKWTFYTAIEVLAALHSMGYIHRDVK 192

QY 224 PENILVDRTHGHIKLVDFGSAAKNSNMKNVNAKPIGTDPYMAPEVLTVNMGCKGTGYGLD 283  
DB 193 PDNMLDISGHIKLADFGTCVMKANGVVRCSAVGTPDYISPEVLNRQGDAB--FGKE 250

QY 284 CDWMSVGVIAEMVYGRSPFAEGTSARTFNINMFQRLKTPDDPKVSSDFDLIQSLLC 343  
DB 251 VDWMSVGVPIYEMVGETFYAEALVSTYINMNHKTSKLPDEPLISTQAKDIKKFLS 310

QY 344 GQKERLKEG---LCCHPFFSKIDN--NIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 311 AAPDLGRNSVDDIRNKKFFVNDWTFATLREASPPVPSLKSDDDTTFEBIEIHRDRDN 370

QY 399 SSPCOLSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSMEK 449  
DB 371 AGDFQL-PKTFNGQLPFPGFTYSNYSVP---KNLLRGHGAGSKONGIEQ 417

RESULT 5  
S74244  
serine/threonine-specific protein kinase (EC 2.7.1.1-) isoform I, Rho-associated - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 16-Aug-2004  
C;Accession: S74244  
R:Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Natsumiya, S.  
FEB5 Lett. 392, 189-193, 1996  
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein  
A;Reference number: S74244; MUID:96368048; PMID:8772201  
A;Accession: S74244  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1354 <NAK>  
A;Cross-references: UNIPROT:P70335; EMBL:U58512; NID:G1514695; PIDN:AAC53132.1; PID:G1514695  
C;Superfamily: protein kinase homology  
C;Keywords: coiled coil; phosphotransferase; serine/threonine-specific protein kinase  
F;74-338/Domain: protein kinase homology <KIN>  
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.3%; Score 866.5; DB 2; Length 1354;  
Best Local Similarity 40.0%; Pred. No. 1.5e-31;  
Matches 186; Conservative 93; Mismatches 157; Indels 29; Gaps 10;

QY 44 SPLSRGILDALFVLFECSQPALMKIKHVSFVRKYSQTIABQLQPSAKDFEVRSLV 103  
DB 23 SEVNSDCLLDGLDALVYDLDFPALRKKNIDNFLSRKYDKTINKIRDLRMKAEDYEVVKVI 82

QY 104 GCCHFAEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSWIPOLQYA 163  
DB 83 GRGAFGEVQLVRHKSTRKYAMKLLSKFEMIKRSASFFWEERDIFAFANSPWVQLFYA 142

QY 164 FQDKNHLVLMVEYQPGDLSILNRYEDQDENLIQFYLAELILAVHSLMGVYHRDIK 223  
DB 143 FQDPRHLYMVEYMPGGDLVNLMSYD--VPEKWARFYTAIEVLAALHSMGYIHRDVK 200

QY 224 PENILVDRTHGHIKLVDFGSAAKNSNMKNVNAKPIGTDPYMAPEVLTVNMGCKGTGYGLD 283  
DB 201 PDNMLDKSGHLKLADFGTCVMKANGVVRCSAVGTPDYISPEVLKSQGD--GYGYRE 258

QY 284 CDWMSVGVIAEMVYGRSPFAEGTSARTFNINMFQRLKTPDDPKVSSDFDLIQSLLC 343  
DB 259 CDWMSVGVFLYEMLVGDTTPFYADSLVGYTSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318

QY 344 GQKERLKEG---LCCHPFFSKIDN--NIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 319 DREVLRGRNGVEEIKRHLFFKNDQWAMETLRDTVAPVVPDLSDDIDTSNFDDEEDKGE 378

QY 399 SS-PCQSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSME--KULLIKS 455

DB 201 PDNMLDKSGHLKLADFGTCVMKANGVVRCSAVGTPDYISPEVLKSQGD--GYGYRE 258

QY 284 CDWMSVGVIAEMVYGRSPFAEGTSARTFNINMFQRLKTPDDPKVSSDFDLIQSLLC 343  
DB 259 CDWMSVGVFLYEMLVGDTTPFYADSLVGYTSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318

QY 344 GQKERLKEG---LCCHPFFSKIDN--NIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 319 DREVLRGRNGVEEIKRHLFFKNDQWAMETLRDTVAPVVPDLSDDIDTSNFDDEEDKGE 378

QY 399 SS-PCQSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSME 448  
DB 379 ETFPI--PKAFVGNQLPFVGFYTSNRRYLPSANSENSSNVDSKLSQESLQKTIYKL 435

QY 449 KKLILKSKELODS--QDKCHKVFISAAGLLPCSRILPSVYAKGSAR 492  
DB 436 BEQLHNEQLKDEMEQKCR-----TSNKLKDKIMKELDEEGNQR 474

RESULT 6  
S69211  
serine/threonine-specific protein kinase (EC 2.7.1.1-), Rho-associated - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 16-Aug-2004  
C;Accession: S69211; S71910  
R:Ishizaki, T.; Maekawa, M.; Fujisawa, K.; Okawa, K.; Iwanatsu, A.; Fujita, A.; Watanabe  
EMBO J. 15, 1885-1893, 1996  
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot  
A;Reference number: S69211; MUID:96203110; PMID:8617235  
A;Accession: S69211  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1354 <ISH>  
A;Cross-references: UNIPROT:Q13464; EMBL:U43195; NID:G1276900; PIDN:AA02814.1; PID:G1276900  
C;Superfamily: protein kinase  
A;Residues: 187-185;281-288;465-473;573-587;818-828;885-893;934-945 <ISH2>  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;74-338/Domain: protein kinase homology <KIN>  
F;82-90/Region: protein kinase ATP-binding motif  
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 33.2%; Score 864.5; DB 2; Length 1354;  
Best Local Similarity 41.1%; Pred. No. 1.8e-31;  
Matches 180; Conservative 89; Mismatches 146; Indels 23; Gaps 9;

QY 44 SPLSRGILDALFVLFECSQPALMKIKHVSFVRKYSQTIABQLQPSAKDFEVRSLV 103  
DB 23 SEVNSDCLLDGLDALVYDLDFPALRKKNIDNFLSRKYDKTINKIRDLRMKAEDYEVVKVI 82

QY 104 GCCHFAEVQVVRKATGDIYAMKMKKALLAQEQVSPFEERNILSRSTSWIPOLQYA 163  
DB 83 GRGAFGEVQLVRHKSTRKYAMKLLSKFEMIKRSASFFWEERDIFAFANSPWVQLFYA 142

QY 164 FQDKNHLVLMVEYQPGDLSILNRYEDQDENLIQFYLAELILAVHSLMGVYHRDIK 223  
DB 143 FQDPRHLYMVEYMPGGDLVNLMSYD--VPEKWARFYTAIEVLAALHSMGYIHRDVK 200

QY 224 PENILVDRTHGHIKLVDFGSAAKNSNMKNVNAKPIGTDPYMAPEVLTVNMGCKGTGYGLD 283  
DB 201 PDNMLDKSGHLKLADFGTCVMKANGVVRCSAVGTPDYISPEVLKSQGD--GYGYRE 258

QY 284 CDWMSVGVIAEMVYGRSPFAEGTSARTFNINMFQRLKTPDDPKVSSDFDLIQSLLC 343  
DB 259 CDWMSVGVFLYEMLVGDTTPFYADSLVGYTSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318

QY 344 GQKERLKEG---LCCHPFFSKIDN--NIRNSPPFPVTLKSDDDTSNFDPEKNSWVS 398  
DB 319 DREVLRGRNGVEEIKRHLFFKNDQWAMETLRDTVAPVVPDLSDDIDTSNFDDEEDKGE 378

QY 399 SS-PCQSPGFSGEELPFVGFYSKALGILGRSESVVSGLDSPAKTSSME--KULLIKS 455



A; Cross-references: UNIPROT: P70336; EMBL: U58513; NID: q1514697; PIDN: AAC53133.1; PID: g1514697; C: Superfamily: protein kinase C zinc-binding repeat homolog; protein kinase homolog; C: Keywords: phosphotransferase; serine/threonine-specific protein kinase F; 50-354/Domain: protein kinase homolog <KIN> F; 1261-1315/Domain: protein kinase C zinc-binding repeat homolog <KZN>

Query Match 32.8%; Score 853.5; DB 2; Length 1388;  
Best Local Similarity 40.0%; Pred. No. 5.7e-31;  
Matches 177; Conservative 95; Mismatches 144; Indels 27; Gaps 9;

QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db																												
32	QKQPPFMTQQMSPLREGILDALFWFFECSPALMKIKHVSNFVKYKSDTIAELQELQ	91	27	QRKLEALIRDRSPINVESLSDGLNSIVLDDFPALRKKNKVIDNFLNRKIVKIRGLQ	86	92	PSAKDFEVSILVCCGHPAEVQVVRKATGDIYAMKWKKALLAQEQVGFEEERNILRS	151	87	MKAEDYDVVKVIIGKGAFAGEVQLVRHKASQVYAMKLLSKPEMIKRGSDSAFFWEERDIMA	146	152	STSPWIPQLQYAFQDKNHLVLMWYQPGDGLLSLNRYEDOLDENLIQVLAELIILAVHS	211	147	ANSPWVQLVFCAPQDRDYIMWMEYMPGGDLVNLMSNYD--VPEKWAKYTAEEVWLALDA	204	212	VHLMGVVHRDIKPNILVDRTGHIKLVDFGSAAKNSKNKMAKLPFGTPTYMAPEVLTV	271	205	IHSWGLIHEDVRKEDPNLLDKHGHLKLADFGTCMKMDETGMVHCDDTAGVPTDVISPEVLKS	264	272	MNGDGKGTGLDCDWMWSGVYAYEMITYGRSPFAEGTSARTFNMINMFORLFLPDDPKVS	331	265	QGGD--GYYGRECDWMWSGVFTPEMLVGDTPFYADSLVGTYSKIMDKHNSCLCFPEDETS	322	332	SDPFLDIQSLLCGQERLKEG--LCCHPEFSKIDWN--NIENSPPPPVPTLKSDDDTS	386	323	KXAKMLICAFLTREVRGRNGVVEETIKQHPFNKNDOWNDNIETAAPVPELSSDDSS	382	387	NFDEPEKNWS--YSSGPCQLSPGSGFGEELPFVFGYSYKALGRSESVVSGLDS--AK	443	383	NFDDIEDDKGDVETPTI---PKAFVGNQLPFIFGYFRENLLS-----DSPPCKR	430	444	TSSMEKKLLIKSKELQDSQDKCH	466	431	NDAIQTR---KSEESOEIOKKLY	450

RESULT 11  
G86431 protein kinase T518.9 protein - Arabidopsis thaliana  
CSpecies: Arabidopsis thaliana (mouse-ear cress)  
CDate: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
CAccession: G86431  
CClassification: Arabidopsis  
RTheologian: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.  
Chen, N.F.; Hughes, B.; Huizar, L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin  
A,Authors: Hunter, J.L.; Li, J.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maith, P.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maith, P.  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A,Reference number: A86141; MUID:21016719; PMID:11130712  
A,Accession: G86431  
A,Status: preliminary  
A,Molecule type: DNA



```

QY 4 PKYGARNP--LDAGAAEPIANRASLNLFQCKPPEMTQQQWSPLSREGILDALFVLFFEE 61
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
265 YMYFERRPDLTLKGTQDKAAAVKUKIENFYOSSVKYAIERNRRVELETEITSNWSBER 324
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 CSOPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEQVQVREKATGD 121
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 KSRQLSSGKSESQFLR-----LRRTRLSLEDFHTVKVIGKAGFCEVRLVQKKDTGK 376
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 IYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGGD 181
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
377 IYAMKTLKSEMYKQDLAHYKARDVLAGSDSPWVSLYYSFQDAQLYLIMEFLPGGD 436
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 LLSLLNRVEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTGHIKLVDFG 241
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
437 LMTWLIRWQ-LFTEDVTRFYNAECILAEITIKLGFTHRDIKPDNILIDIRGHIKLSDFG 495
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 -----SAAKNSN----- 249
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
496 LSTGFKTHDSNYKKLLQDDEATNGISKPGTYNANTTDTANKRQTMVVDISLTMNRQ 555
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
250 -----KMVNAKLPIGTDPYMAPEVLTVNMGDGKTYGLDCDWSVGVIAVEMYIGRS 301
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
556 QIOTWRKSRRLMAYSTVGTDPYIAPEIFYG-----YGOECDWWSLGAIMEYCLIGWP 609
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 PFASGTSARTFNNTMNFQRLKFPDDPKVASDFDLIQSLILCGOKERLKPEG-----LCCH 357
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
610 PFCSETQETRYKTNFQETLQFPDDLHISYEADLIRLLTHADQRLGRHGGADEIKSH 669
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
358 PFFSKIDWNINRSPFPFVPTLKSDDTSNFDPEKNSWYSSGPC-----QLSPSG 408
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
670 PFRFGVDWNTIRQVEAIVPKLSIITRFFPTDELEN-VPDSPAMAQAQAQEQMTKQG 728
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
409 FSG---BELPFGFSYSK 423
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
729 GSAPVKEDLPFGITYSR 746

RESULT 14
S49077
protein kinase PCTL7 (EC 2.7.1.-) - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 31-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C/Accession: S49077
R:Huang, Y.; Wan, J.; Ko, K.; Dennis, D.T.
submitted to the EMBL Data Library, December 1992
A:Description: A CAMP-dependent protein kinase homolog in tobacco leaf.
A:Reference number: S49077
A:Accession: S49077
A:Molecule type: mRNA
A:Residues: 1-526 <HUA>
A/Cross-references: UNIPROT:Q40547; EMBL:X71057; NID:G506533; PID:G5065
C/Superfamily: Arabidopsis thaliana protein kinase TSI8.9; protein kinase homology
C/Keywords: ATP; phosphotransferase; protein kinase
F:109-420/Domain: protein kinase homology <KIN>
F:117-125/Region: protein kinase ATP-binding motif

Query Match 26.9%; Score 701; DB 2; Length 526;
Best Local Similarity 35.9%; Pred. No. 1.4e-24;
Matches 160; Conservative 74; Mismatches 144; Indels 68; Gaps 8;

QY 76 FVRKYSDDTIAELQELQPSAKDFEVRSLVCGCHFAEV-----QVVRKATGDIVA 124
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
90 FLEKKETEYWRJQRHKGAGDDPELLTMIKGAFGEPICMGFSVITGQNCREKTTGQVYA 149
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 MKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGGDLLS 184
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
150 MKKLKSEMLRRQGVHVAERNLLAEVSDCIKLYISFQDDDLVLYLWVEYFGDDMT 209
QY      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 LLNRVEDQDENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTGHIKLVDFGSA 244
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
210 LLMR-KDILTEADPARYVAETVLATESISKHNYIHRDIKPDNLLIDRYGHKLSPGLCK 268

```

QY 245 KVN-----SNKVNAKLPIGTPDYMA 265  
Db 269 PLDCSTLBEKDFSGVDNANGGSRDSPAPKRTQOELEHWQKRRMLAYSTVGTPDYIA 328  
QY 266 PEVLTMWNGDGKGTGLDCDWMKSVGVIAEMVIGSRSPFAEGTSARTFNNIMNFQRELKEP 325  
Db 329 PEVLL-----KXGYGMECDWWSLGAIMYEMLVGPPFVSDPDMSTCRKIVNWKHLKRP 382  
QY 326 DDPKVSDFDLIOQLCGQKRLKFEK---LCCHFFFSKIDNNIRNSPPFPVPTLKSD 382  
Db 383 EEAKLSPKADIIIRLLCNVTERLGSNGADEIKVHSWFKGIDWDRIYQMEAAFIPEVND 442  
QY 383 DDTSNFDEPEKNSVSWSPCQLSP---SFSCEBELPFVCFYSKALGILGRSSVSVGLDS 440  
Db 443 LDTQNFERFEESHSQSGSRGPRKWLSSKDNFVGYTKNFKV---NDYQVPGMVE 499  
QY 441 PAKTSSMEKLLIKS---KELQDSOD 463  
Db 500 LKKTNTKPKPTIKSLFGDESEASED 525  
RESULT 15  
T41723  
serine/threonine-specific protein kinase (EC 2.7.1.-) orb6 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
C:Accession: T41723; T43526  
R:Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z22012  
A:Accession: T41723  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-469 <R1E>  
A:Cross-references: UNIPROT:O13310; EMBL:AL4121770; PIDN:CAE57446.1; GSPDB:GN000000000  
A:Experimental source: strain 972h-; cosmid c821  
R:Verde, F.; Wiley, D.J.; Nurse, P.  
Proc. Natl. Acad. Sci. U.S.A. 95, 7526-7531, 1998  
A:Title: Fission yeast orb6, a ser/thr protein kinase related to mammalian rho th the cell cycle.  
A:Reference number: Z22544; MUID:98301608; PMID:9636183  
A:Accession: T43526  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-469 <VER>  
A:Cross-references: EMBL:AF009512; NID:G2443510; PIDN:AAC32420.1; PID:G2443511  
C:Genetics:  
A:Gene: orb6; SPAC821.12  
A:Map position: 1  
A:Introns: 48/2; 106/3  
C:Function:  
A:Description: coordinates maintenance of cell polarity during interphase with  
A>Note: interacts genetically with orb2, which encodes the Pak1/Shk1 protein kin  
C:Superfamily: protein kinase homology  
C:Keywords: phosphotransferase

```

Query Match      26.9%; Score 700; DB 2; Length 469;
Best Local Similarity 39.2%; Pred. No. 1.4e-24;
Matches 148; Conservative 63; Mismatches 113; Indels 54; Gaps 8;

QY 93 SAKDFEVRSLVGGCHFAEYQVVEKATGDTIYAMKVMKKKALLAQEQVSPFEERNILSR 152
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 SLEDFSTIKVIGKAGEVRLVQKLTGKLIYAMKSLKTEFKRQDUAHKAERDLIVES 148
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 153 TSPWIPOLQYAFODKNHLYLVMEYQPGGDLSSLNRYEDLDENLIQFYLAELITLAVHS 212
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 DSPWVVSLYYAFODSLYLYLIMEFLPGGLMTMLINY-DTFSEDTVTRFYMAECVLATDV 207
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 213 HLMGYVHRDIKPNILVADRTGHIKLVDFG-----SAAKM----- 246
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 HRMGYVHRDIKPNILIDRDGHIKLSDFGLSTGFYQDOSASVYMKPRTGNTVKRGQWDA 267
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 247 -----NSNKMVMNAKLPIGTGPDYMAPEVLTVNMGDGKGTYGILDCDWWSGVVI 292
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Fri Nov 12 12:26:07 2004

Db	268	IWLTSSKDKMATWKNRRVMAYSTVGTDPDYIAPEIF-LQOG-----YQDCDWWSLGAI	321
Qy	293	AYEMMYGRSFFAEGTSARTFNNMFPORFLKFPDDPKVSSDFDLIQSLLCQOKERLKPE	352
Db	322	MPECLIGWPPFCSENSHETYRKIIINWRETITFPENDIHLSIEARDLMDRLMTDSEHRLGRG	381
Qy	353	G---LCCHPFFSKIDWNNIRNSPPPEVPTLKSDDDTSNF--DEPEK--NSWYSSSPCOLS	405
Db	382	GAIEIMQHFFFTGIDWDHIRETAAPFIPNLKSIITDTHYFPVDELEQVPEQPVTQOPASVD	441
Qy	406	PSGFSGEELPFVGFYSYK	423
Db	442	POTLEQTNLAFGLGYTKK	459

Search completed: November 8, 2004, 12:32:19  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 8, 2004, 12:18:30 ; Search time 156 Seconds  
(without alignments)  
1142.875 Million cell updates/sec

Title: US-10-724-594-2

Perfect score: 2602

Sequence: 1 MLKFKYGARPLDAGRAEPI.....CSRILPSVYAKGARGCWL 497

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2602	100.0	497	6	ABU10126
2	2602	100.0	497	7	Aae39504 Human kin
3	2602	100.0	497	8	Ado40592 Human kin
4	2597	99.8	497	6	ABP97687
5	2589	99.5	497	5	Aae16261 Amino aci
6	2589	99.5	497	6	ABU16261 Human kin
7	2582	99.2	495	6	ABU10127 Variant n
8	2440	93.8	620	6	ABP97681 Amino aci
9	2440	93.8	620	8	ADN62809 Human NOV
10	2440	93.8	623	6	ADA05644 Human NOV
11	2440	93.8	1958	5	ABBS1928 Human kin
12	2440	93.8	2054	5	ABBS1927 Human kin
13	2440	93.8	2054	5	Aae24150 Human kin
14	2430	93.4	2053	6	AAO26959 Human CRI
15	2430	93.4	2053	7	Aae24079 Human MDP
16	2418.5	92.9	2053	4	ADP60994 Pain aso
17	2418.5	92.9	2055	8	AAU03501 Human pro
18	2412.5	92.7	2053	5	ADJ96610 Human cit
19	2412.5	92.7	2053	5	ABG78363 RHO/RAC-i
20	2412.5	92.7	2053	6	ADA05642 Human NOV
21	2412.5	92.7	2053	8	ADN63228 Human NOV
22	2412.5	92.7	2053	8	ADN62807 Human NOV
23	2412.5	92.7	2066	5	ABG78362 Human pro
24	2400.5	92.3	2066	6	ADA05654 Human NOV
25	2271.5	87.3	494	6	ABP97682 Polypepti

26	2271.5	87.3	494	8	ADO40594	Ado40594 Mouse cit
27	2172.5	83.5	2055	6	ABP97683	Abp97683 Polypepti
28	2172.5	83.5	2055	6	AAO26950	Aao26950 Human CRI
29	1652	63.5	319	7	ADN62730	Adn62730 Human cit
30	1627	62.5	349	4	ABG15566	Abg15566 Novel hum
31	1284	49.3	257	7	ADJ79947	Adj79947 Human kin
32	1180	45.3	251	7	ADJ79949	Adj79949 Rat kinas
33	1177	45.2	251	7	ADJ79950	Adj79950 Mouse kin
34	932.5	35.8	1565	8	ADP47967	Adp47967 Human MRC
35	929	35.7	475	5	AAE24131	Aae24131 Human kin
36	929	35.7	1197	6	ABJ37881	Abj37881 NOVX prot
37	929	35.7	1247	6	ABJ37882	Abj37882 NOVX prot
38	929	35.7	1551	8	ADJ40850	Adj40850 Human kin
39	929	35.7	1553	7	ADG99064	Adg99064 Human KPP
40	929	35.7	1569	8	ADP95102	Adp95102 Human ser
41	929	35.7	1572	5	AAE19162	Aae19162 Human kin
42	929	35.7	1572	8	ADJ96611	Adj96611 Human dys
43	926	35.6	1548	8	ADP95100	Adp95100 Human ser
44	922	35.4	1252	4	ABB66357	Abb66357 Drosophil
45	896.5	34.5	1000	7	ADB82759	Adb82759 Human pro

## ALIGNMENTS

RESULT 1  
ABU10126  
ID ABU10126 standard; protein; 497 AA.  
XX AC ABU10126;  
XX AC  
DT 11-AUG-2003 (first entry)  
XX DE Novel human kinase.  
XX KW Human; enzyme; gene therapy; kinase; antisense.  
XX OS Homo sapiens.  
XX PN US2003022340-A1.  
XX PD 30-JAN-2003.  
XX PF 11-SEP-2002; 2002US-00238709.  
XX PR 13-MAR-2001; 2001US-00804471.  
XX PA (APPL-) APPLERA CORP.  
XX PI Webster M, Van C, Di Francesco V, Beasley EM;  
DR WPI; 2003-438978/41.  
DR N-P5DB; ACA61394.  
PT New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.  
PT Claim 1; Fig 2; 207pp; English.  
CC The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase.  
CC The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for

CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the transporter gene in clinical trials or in treatment  
 CC regimen, in gene therapy and as antisense constructs to control  
 CC transporter gene expression in cells, tissue and organisms. The present  
 CC sequence represents the amino acid sequence of a novel human kinase  
 XX  
 SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 6; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAPIANRSLNLFQGGPMTQOQMSPLREGILDALVLFEE 60  
 Db 1 MLKFKYGARNPLDAGAAPIANRSLNLFQGGPMTQOQMSPLREGILDALVLFEE 60  
 QY 61 ECSQPALMKIKHVSFNFKYSDTIAELQELQPSAKDFEVSRLVCGGFAEVQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFNFKYSDTIAELQELQPSAKDFEVSRLVCGGFAEVQVREKATG 120  
 QY 121 DIYAMKVMKKALLAQEQVSFEERNILGRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 Db 121 DIYAMKVMKKALLAQEQVSFEERNILGRSTSPWIPOLQYAFQDKNHLVLMVEYQPG 180  
 QY 181 DLLSLNRYEQDENLIQFYLAELIIVSHVLMGVVHRDIKPNILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEQDENLIQFYLAELIIVSHVLMGVVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAKMSNKMVNKAKLPIGTDPYAPVLTVMNGDGKGTGLDCDMSVGVIAEYMIYGR 300  
 Db 241 GSAKMSNKMVNKAKLPIGTDPYAPVLTVMNGDGKGTGLDCDMSVGVIAEYMIYGR 300  
 QY 301 SPFAEGTSARTFNIMNFORLKPDPKVSDFDLIQSLCGQKRLKFEGLCHPFF 360  
 Db 301 SPFAEGTSARTFNIMNFORLKPDPKVSDFDLIQSLCGQKRLKFEGLCHPFF 360  
 QY 361 SKIDWNNIRNSPPFPVPTLTKSDDTNSFNDEPEKNSVSSPCQLSPGSGBELPVGFS 420  
 Db 361 SKIDWNNIRNSPPFPVPTLTKSDDTNSFNDEPEKNSVSSPCQLSPGSGBELPVGFS 420  
 QY 421 YSKALGILGRESVVGSLDPAKTSMEKLLIKSKELQDSQDKCHKVFIISAAGLLPCSR 480  
 Db 421 YSKALGILGRESVVGSLDPAKTSMEKLLIKSKELQDSQDKCHKVFIISAAGLLPCSR 480  
 QY 481 ILPSVYAKSGARGCWL 497  
 Db 481 ILPSVYAKSGARGCWL 497

RESULT 2  
 AAE39504  
 ID AAE39504 standard; protein; 497 AA.  
 XX  
 AC AAE39504;  
 XX

DT 18-DEC-2003 (first entry)

DE Human kinase protein.

KW Human; kinase protein; diagnostic; therapeutic; immune response; enzyme;  
 KW pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic.  
 OS Homo sapiens.

FT Key Location/Qualifiers  
 FT Modified-site 50..55  
 FT /note= "N-myristoylation site"  
 FT Modified-site 78..81  
 FT /note= "cAMP and cGMP dependent protein kinase  
 FT phosphorylation site"  
 FT Modified-site 83..86  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site 93..96

FT Modified-site  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 93..96  
 FT /note= "Protein kinase C phosphorylation site"  
 FT 103..126  
 FT /note= "Protein kinase Atp-binding region signature"  
 FT 140..143  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT 197..217  
 FT /note= "Helix I"  
 FT Active-site  
 FT 217..229  
 FT /note= "Serine/Threonine protein kinase active-site  
 FT signature"  
 FT 248..250  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site  
 FT 308..310  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site  
 FT 361..364  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Misc-difference  
 FT 365  
 FT /note= "This residue changes to Cys during single  
 FT nucleotide polymorphism (SNP)"  
 FT Modified-site  
 FT 378..380  
 FT /note= "Protein kinase C phosphorylation site"  
 FT Modified-site  
 FT 381..384  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site  
 FT 386..389  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site  
 FT 410..413  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site  
 FT 436..439  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Modified-site  
 FT 445..448  
 FT /note= "Caesin kinase II phosphorylation site"  
 FT Region  
 FT 467..487  
 FT /note= "Helix II"  
 FT Modified-site  
 FT 474..479  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 489..494  
 FT /note= "N-myristoylation site"  
 FT Modified-site  
 FT 490..492  
 FT /note= "Protein kinase C phosphorylation site"  
 FT  
 FN US2002132322-A1.  
 XX 19-SEP-2002.  
 XX  
 XX 13-MAR-2001; 2001US-00804471.  
 XX  
 XX 13-MAR-2001; 2001US-00804471.  
 XX  
 XX (WEBS/) WEBSTER M.  
 XX (VANC/) YAN C.  
 XX (DPRA/) DI FRANCESCO V.  
 XX (BEAS/) BEASLEY E M.  
 XX  
 XX Webster M, Yan C, Di Francesco V, Beasley EM;  
 XX  
 XX WPI; 2003-687480/65.  
 XX N-PSDB; AAD59937, AAD59938.  
 XX  
 XX New isolated human kinase proteins, useful as models for developing human  
 XX therapeutic targets, or for treating a disorder associated with an  
 XX absence of, inappropriate or unwanted expression of the protein, e.g.  
 XX cancer.  
 XX  
 XX Claim 1; Fig 2; Opp; English.  
 XX  
 XX The present invention relates to human kinase proteins and nucleic acids  
 XX encoding them all of which are useful in the development of human  
 XX therapeutics and diagnostic composition and methods. The invention is  
 XX useful as models for the development of human therapeutic targets, aid in  
 XX the identification of therapeutic proteins and serve as targets for the  
 XX development of human therapeutic agents. The invention is also useful in



CC drug screening assays, in assays to determine the biological activity of  
 CC the protein, to raise antibodies and to elicit another immune response.  
 CC The antibodies are useful in pharmacogenomic analysis, for inhibiting  
 CC protein function and for tissue typing. The transgenic animals are useful  
 CC for studying the function of kinase protein, identifying and evaluating  
 CC modulators of kinase protein activity. The invention is also used in gene  
 CC therapy. The present sequence is the human kinase protein. The human  
 CC kinase gene is located on chromosome 12  
 XX  
 SQ Sequence 497 AA;

Query Match 100.0%; Score 2602; DB 7; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e-254;  
 Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLKFKYGARPLDAGAEPTANRASRLNLFQKPPFTQOQMSPLSREGILDALFVLFE	60
Db	1	MLKFKYGARPLDAGAEPTANRASRLNLFQKPPFTQOQMSPLSREGILDALFVLFE	60
Qy	61	ECSPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG	120
Db	61	ECSPALMKIKHVSFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVRKATG	120
Qy	121	DIYAMKMKKALLAQOVQSFPEERNILSRSTSPWIPQIYAFQDKNHLVLMYEQPG	180
Db	121	DIYAMKMKKALLAQOVQSFPEERNILSRSTSPWIPQIYAFQDKNHLVLMYEQPG	180
Qy	181	DLASLLNRYEDQDENLIQYLAELILAVHSVHMGVVRHDIKPNILVDRTHIKLVDF	240
Db	181	DLASLLNRYEDQDENLIQYLAELILAVHSVHMGVVRHDIKPNILVDRTHIKLVDF	240
Qy	241	GSAAKMNSKQVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWWSGVIAEMYGR	300
Db	241	GSAAKMNSKQVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWWSGVIAEMYGR	300
Qy	301	SPRAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCCQKRLKFEGLCCHPFF	360
Db	301	SPRAEGTSARTFNINMFORFLKFPDDPKVSSDFLDLIQSLCCQKRLKFEGLCCHPFF	360
Qy	361	SKIDMNNIRNSPPFPVPTLTKSDDDTSNFDPEKNSWSSPQOLSPSGFSGEELPFVGS	420
Db	361	SKIDMNNIRNSPPFPVPTLTKSDDDTSNFDPEKNSWSSPQOLSPSGFSGEELPFVGS	420
Qy	421	YSKALGILGRSESVSGLSPAKTSMEKLLIKSKELQSDQKCHKVFIISAAGLLPCSR	480
Db	421	YSKALGILGRSESVSGLSPAKTSMEKLLIKSKELQSDQKCHKVFIISAAGLLPCSR	480
Qy	481	ILPSVYAKGSARGCWL 497	
Db	481	ILPSVYAKGSARGCWL 497	

RESULT 3  
 ADO40592  
 ID ADO40592 standard; protein; 497 AA.  
 XX  
 AC ADO40592;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human kinase protein.  
 XX  
 KW Kinase; rho/rac-interacting citron kinase; drug screening;  
 KW kinase related disorder; human; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 50..55  
 FT Modified-site /note= "N-myristoylation site"  
 FT Modified-site 78..81  
 FT /note= "cAMP and cGMP dependent protein kinase  
 FT phosphorylation site"

FT	Modified-site	83..86	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	93..96	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	93..95	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	103..126	/note= "protein kinase C phosphorylation site"
FT	Binding-site	140..143	/note= "protein kinase ATP-binding region signature"
FT	Modified-site	140..143	/note= "Casein kinase II phosphorylation site"
FT	Region	197..217	/note= "Helix 1"
FT	Active-site	217..229	/note= "Serine/Threonine protein kinase active-site signature"
FT	Modified-site	248..250	/note= "protein kinase C phosphorylation site"
FT	Modified-site	308..310	/note= "protein kinase C phosphorylation site"
FT	Modified-site	361..364	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	378..380	/note= "protein kinase C phosphorylation site"
FT	Modified-site	381..384	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	386..389	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	410..413	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	436..439	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	445..448	/note= "Casein kinase II phosphorylation site"
FT	Region	467..487	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	474..479	/note= "N-myristoylation site"
FT	Modified-site	489..494	/note= "N-myristoylation site"
FT	Modified-site	490..492	/note= "Protein kinase C phosphorylation site"

US2004091993-A1.

13-MAY-2004.

02-DEC-2003; 2003US-00724594.

13-MAR-2001; 2001US-00804471.

11-SEP-2002; 2002US-00238709.

(APPL-) APPLERA CORP.

Webster M, Yan C, Di Francesco V, Beasley EM;

WPI; 2004-374957/35.

N-ESDB; ADO40591, ADO40593.

New isolated human kinase proteins and nucleic acids, useful for developing human therapeutic targets, identifying therapeutic proteins or serve as targets for the development of human therapeutic agents that modulate kinase activity.

Claim 1; SEQ ID NO 2; 207pp; English.

The present invention provides a kinase polypeptide and its encoding polynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases, in drug screening assays, for treating disorders characterized by an absence of inappropriate and



ID	AAE16261	standard; protein; 497 AA.
XX	AC	AAE16261;
XX	DT	26-MAR-2002 (first entry)
XX	DE	Human kinase PKIN-7 protein.
XX	KW	Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis;
XX	KW	immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
XX	KW	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
XX	KW	allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
XX	KW	autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis;
XX	KW	Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
XX	KW	rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
XX	KW	hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
XX	KW	cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
XX	KW	congestive heart failure; ischaemic heart disease; lung tumour; gout;
XX	KW	fatty liver; Niemann-Pick's disease; gene therapy.
OS	Homo sapiens.	
PH	Key	Location/Qualifiers
FT	Domain	86..124
FT	Domain	/label= Protein_kinase_domain
FT	Domain	96..153
FT	Domain	/label= Protein_kinase_domain
FT	Domain	97..360
FT	Domain	/note= "Eukaryotic protein kinase domain"
FT	Domain	98..241
FT	Domain	/label= Protein_kinase_domain
FT	Domain	99..349
FT	Domain	/label= Protein_kinase_domain
FT	Domain	101..241
FT	Domain	/label= Protein_kinase_domain
FT	Domain	102..241
FT	Domain	/label= Protein_kinase_domain
FT	Domain	249..349
FT	Domain	/label= Protein_kinase_domain
FT	Domain	258..445
FT	Domain	/label= Protein_kinase_domain
FT	Domain	258..349
FT	Domain	/label= Protein_kinase_domain
FT	Domain	361..390
FT	Domain	/note= "Protein kinase C terminal domain"
XX	WO200196547-A2.	
XX	20-DEC-2001.	
XX	14-JUN-2001; 2001WO-US019444.	
XX	15-JUN-2000; 2000US-0212073P.	
XX	23-JUN-2000; 2000US-0213467P.	
XX	30-JUN-2000; 2000US-0215651P.	
XX	07-JUL-2000; 2000US-0216605P.	
XX	13-JUL-2000; 2000US-0218372P.	
XX	25-AUG-2000; 2000US-0228056P.	
XX	(INCY-) INCYTE GENOMICS INC.	
XX	Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y,	
XX	Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DAM, Greenwald SR;	
XX	Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;	
XX	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;	
XX	Lo TP, Khan F, Recipon SA, Azinzai Y, Policky JL, Ding L;	
XX	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;	
XX	WPI: 2002-090207/12.	
XX	N-PSDB; AAD26454.	
XX	New polypeptides, useful for diagnosing, treating or preventing disorders	
XX	of growth and development, cardiovascular and lipid, and diseases such as	
PT	cancer, comprise human kinase polypeptides.	
XX	Claim 1; Page 146-147; 197pp; English.	
XX	The invention relates to human kinase PKIN proteins and their	
XX	corresponding cDNAs. A composition containing PKIN agonist is useful for	
XX	treating a disease or condition associated with decreased expression of	
XX	PKIN and a composition comprising PKIN antagonist is useful for treating	
XX	a disease or condition associated with overexpression of PKIN. The	
XX	disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,	
XX	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder	
XX	(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,	
XX	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,	
XX	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes	
XX	mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,	
XX	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's disease,	
XX	rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,	
XX	bacterial, parasitic, fungal, viral, protozoal and helminthic infections,	
XX	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,	
XX	Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio	
XX	vascular disease (arteriovenous fistula, hypertension, vasculitis,	
XX	aneurysms, congestive heart failure, angina pectoris, myocarditis,	
XX	ischaemic heart disease, chronic bronchitis, lung tumours); lipid	
XX	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,	
XX	hypercholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity	
XX	of a test compound and in gene therapy. The present sequence is human	
XX	PKIN-7 protein	
SQ	Sequence 497 AA;	
Query Match	99.5%; Score 2589; DB 5; Length 497;	
Best Local Similarity	99.6%; Pred. No. 4.2e-253;	
Matches	495; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQGGPPPTQOQMSPLREGILDALFVLF 60	
DB	1 MLKFKYGARNPLDAGAAEPTANRASRLNLFQGGPPPTQOQMSPLREGILDALFVLF 60	
QY	61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGHFAEVQVREKATG 120	
DB	61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGHFAEVQVREKATG 120	
QY	121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQLOAYAFQDKNHLVLMVEYOPGG 180	
DB	121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQLOAYAFQDKNHLVLMVEYOPGG 180	
QY	181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240	
DB	181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVVHRDIKPENILVDRTHIKLVDF 240	
QY	241 GSAAKNSNKNVNAKLPDGTDPYVAPVLTVMNGDGKTYGLDCDMSVGVIAIYMIYGR 300	
DB	241 GSAAKNSNKNVNAKLPDGTDPYVAPVLTVMNGDGKTYGLDCDMSVGVIAIYMIYGR 300	
QY	301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFLDLIQSLLCGKERLKEGCLCHPFF 360	
DB	301 SPFAEGTSARTFNINMNFQFLKFPDDPKVSSDFLDLIQSLLCGKERLKEGCLCHPFF 360	
QY	361 SKIDMNNIRNSPPFPVPTLKSDDDTNFDPEFNKNVSSSPCQLSPSGFSGEELPFVGF 420	
DB	361 SKIDMNNIRNSPPFPVPTLKSDDDTNFDPEFNKNVSSSPCQLSPSGFSGEELPFVGF 420	
QY	421 YSKALGILGHSESVSGLOSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAGLLPCSR 480	
DB	421 YSKALGILGHSESVSGLOSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAGLLPCSR 480	
QY	481 ILPSVYAKGSARGRCWL 497	
DB	481 ILPSVYAKGSARGRCWL 497	
RESULT 6		
ABU10127		

Db	121	DIYAMKVMKKALLAQEQVGFEEERNILSRSTSPWIPQLQYAFQDKNHLILVMYIQGG	180		
QY	181	DLLSLLNRYEDQDENLIIQYLAEELIAVHSHVLMGYVHRDIKPENILVDRTHIKLVDF	240		
Db	181	DLLSLLNRYEDQDENLIIQYLAEELIAVHSHVLMGYVHRDIKPENILVDRTHIKLVDF	240		
QY	241	GSAAKMSNKQVNAKLPIGTDPDYMAPEVLTVWNGDGKGYGLDCDWSVGVYAYEMIXGR	300		
Db	241	GSAAKMSNKQVNAKLPIGTDPDYMAPEVLTVWNGDGKGYGLDCDWSVGVYAYEMIXGR	300		
QY	301	SPRAGTSARTFNINMFQFLKFPDDPKVSSDFDLIIQSLLCGGKXERLKFEGLCCHPFF	360		
Db	301	SPFAGTSARTFNINMFQFLKFPDDPKVSSDFDLIIQSLLCGGKXERLKFEGLCCHPFF	360		
QY	361	SKIDWNINRSPFPFVPTLKSDDTNSNFDPEKSNWSSSPQLSPSGSGSELFPVGFS	420		
Db	361	SKIDCNNINRSPFPFVPTLKSDDTNSNFDPEKSNWSSSPQLSPSGSGSELFPVGFS	420		
QY	421	YSKALGILGRSESVVSLGDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR	480		
Db	421	YSKALGILGRSESVVSLGDSPAKTSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR	480		
QY	481	ILPSVYAKSGARGCWL	497		
Db	481	ILPSVYAKSGARGCWL	497		
RESULT 7					
ID	ABP97681				
ID	ABP97681	standard; protein; 495 AA.			
AC	ABP97681;				
XX					
DT	16-MAY-2003	(first entry)			
DE	Amino acid sequence of citron rho/rac-interacting kinase-short kinase.				
KW	Human: citron rho/rac-interacting kinase-short kinase; obesity;				
KW	chronic obstructive pulmonary disease; hypertension; diabetes;				
KW	coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;				
KW	gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;				
XX	polycystic ovarian syndrome; fertility; depression.				
OS	Homo sapiens.				
EN	W02003004629-A2.				
XX					
PD	16-JAN-2003.				
XX					
PF	01-JUL-2002; 2002WO-EP007229.				
XX					
PR	02-JUL-2001; 2001US-0301853P.				
PR	10-DEC-2001; 2001US-0337130P.				
PR	25-APR-2002; 2002US-0375015P.				
XX					
PA	(FARB ) BAYER AG.				
XX					
PI	Zhu Z;				
XX					
DR	WPI; 2003-221595/21.				
DR	N-PSDB; AB268725.				
XX					
PT	New human citron rho/rac-interacting kinase-short kinase polypeptide and				
PT	polynucleotide for preventing or treating diseases associated with the				
PT	polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary				
PT	disease.				
XX					
PS	Claim 1; Fig 2; 145pp; English.				
XX					
CC	The present sequence represents a human citron rho/rac-interacting kinase				
CC	-short kinase polypeptide. The polynucleotide and polypeptide of the				
CC	invention are useful in preventing, ameliorating, or treating diseases				

CC associated with the polypeptide dysfunction. The expression vector or the  
 CC reagent is useful in the preparation of a medicament for modulating the  
 CC activity of a human citron rho/rac-interacting kinase-short kinase in a  
 CC disease, such as obesity or chronic obstructive pulmonary disease. These  
 CC may also be used for treating obesity/ overweight-associated  
 CC comorbidities, such as hypertension, diabetes, coronary artery disease,  
 CC hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep  
 CC apnea, cancer, thrombotic diseases, polycystic ovarian syndrome, reduced  
 CC fertility, and depression  
 XX  
 SQ Sequence 495 AA;

Query Match 99.2%; Score 2582; DB 6; Length 495;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-252;  
 Matches 494; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLKPKYGARNFLDAGAEPIANRASRLNLFQGGPPPTQOQMSPLSREGILDALFVLFE 60  
 DB 1 MLKPKYGARNFLDAGAEPIANRASRLNLFQGGPPPTQOQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSNFVKYSDDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120  
 DB 61 ECSQPALMKIKHVSNFVKYSDDTIAELQELQPSAKDFEVRSLVCGGHFAEVQVREKATG 120  
 QY 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPG 180  
 DB 121 DIYAMKVMKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMYEQPG 180  
 QY 181 DLLSLNRYEOLDENLIQFYLABLILAVHSVHLMGVVHRDIPENILVDRTGHIKLVDF 240  
 DB 181 DLLSLNRYEOLDENLIQFYLABLILAVHSVHLMGVVHRDIPENILVDRTGHIKLVDF 240  
 QY 241 GSAAKNKNKVMNAKLPICTPDYMAPEVLTVMNGDGKGTGVLCDMDWSVGVIAEYMIYGR 300  
 DB 241 GSAAKNKNKVMNAKLPICTPDYMAPEVLTVMNGDGKGTGVLCDMDWSVGVIAEYMIYGR 300  
 QY 301 SPFAEGTSGARTFNNIMNFORLKPDPDKYSSDPLDLIQSLCCQERLAFEGLCCHPFF 360  
 DB 301 SPFAEGTSGARTFNNIMNFORLKPDPDKYSSDPLDLIQSLCCQERLAFEGLCCHPFF 360  
 QY 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPFCQLSPFGSGEELPFVGF 420  
 DB 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFDPEKNSWSSPFCQLSPFGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVGLDSDPAKTSMEKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 DB 421 YSKALGILGRSESVVGLDSDPAKTSMEKLLIKSKELQSDQKCHKVFISAAGLLPCSR 480  
 QY 481 ILPSVYAKGSARGC 495  
 DB 481 ILPSVYAKGSARGC 495

RESULT 8  
 ADN62809  
 ID ADN62809 standard; protein; 620 AA.

AC ADN62809;

XX 01-JUL-2004 (first entry)

DE Human NOV1b.

KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;  
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; immune disorder;  
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;  
 KW wasting disorder.

XX Homo sapiens.

OS US2004038223-A1.

XX

PD 26-FEB-2004.  
 XX 01-OCT-2002; 2002US-00262511.  
 XX 02-OCT-2001; 2001US-0326483P.  
 PR 05-OCT-2001; 2001US-0327435P.  
 PR 05-OCT-2001; 2001US-0327449P.  
 PR 09-OCT-2001; 2001US-0327917P.  
 PR 09-OCT-2001; 2001US-0328029P.  
 PR 09-OCT-2001; 2001US-0328044P.  
 PR 09-OCT-2001; 2001US-0328056P.  
 PR 12-OCT-2001; 2001US-0328849P.  
 PR 15-OCT-2001; 2001US-0329414P.  
 PR 17-OCT-2001; 2001US-0330142P.  
 PR 18-OCT-2001; 2001US-0330309P.  
 PR 22-OCT-2001; 2001US-0341058P.  
 PR 24-OCT-2001; 2001US-0339266P.  
 PR 24-OCT-2001; 2001US-0343629P.  
 PR 29-OCT-2001; 2001US-0349575P.  
 PR 01-NOV-2001; 2001US-0346357P.  
 PR 17-APR-2002; 2002US-0373260P.  
 PR 19-APR-2002; 2002US-0373815P.  
 PR 19-APR-2002; 2002US-0373817P.  
 PR 19-APR-2002; 2002US-0373826P.  
 PR 19-APR-2002; 2002US-0373884P.  
 PR 22-APR-2002; 2002US-0374977P.  
 PR 16-MAY-2002; 2002US-0381037P.  
 PR 16-MAY-2002; 2002US-0381038P.  
 PR 16-MAY-2002; 2002US-0381042P.  
 PR 17-MAY-2002; 2002US-0381642P.  
 PR 28-MAY-2002; 2002US-0383656P.  
 PR 29-MAY-2002; 2002US-0383831P.  
 PR 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.  
 PA (MILL/) MILLET I.  
 PA (PEYM/) PEYMAN J. A.  
 PA (KEND/) KEKUDA R.  
 PA (JUGJ/) JU J.  
 PA (LILL/) LI L.  
 PA (GUOX/) GUO X.  
 PA (PATT/) PATTURAJAN M.  
 PA (SPVT/) SPYTEK K. A.  
 PA (EDIN/) EDINGER S. R.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U. M.  
 PA (ORTT/) ORT T.  
 PA (GORM/) GORMAN L.  
 PA (ZERH/) ZERHUSEN B. D.  
 PA (ANDE/) ANDERSON D. W.  
 PA (ZHON/) ZHONG M.  
 PA (CATT/) CATTERTON E.  
 PA (JIWW/) JI W.  
 PA (MILL/) MILLER C. E.  
 PA (RAST/) RASTELLI L.  
 PA (STON/) STONE D. J.  
 PA (PENA/) PENA C. E. A.  
 PA (SHEN/) SHENOY S. G.  
 PA (SHIM/) SHIMKETS R. A.  
 PA (ROTH/) ROTHENBERG M. E.  
 PA (LEAC/) LEACH M. D.  
 PA (AGEE/) AGEE M. L.  
 PA (BERG/) BERGHS C.  
 PA (DIPI/) DIPIPO V. A.  
 PA (EISE/) EISEN A.  
 PA (GANG/) GANGOLLI E. A.  
 PA (RIEG/) RIEGER D. K.  
 PA (SPAD/) SPADERNA S. K.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
 PI Patturajan M, Spytek K, Ellerman K, Malyankar UM;  
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;  
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;

Fri Nov 12 12:26:05 2004

us-10-724-594-2.rag

PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;  
XX  
XX  
XX WPI: 2004-213931/20.  
DR N-PSDB; ADM62808.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,  
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.  
XX  
XX  
XX Claim 1; SEQ ID NO 4; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.  
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or  
CC treat a medical condition in human related to the aberrant expression and  
CC activity of NOVX polypeptides. For example, NOVX polypeptides and  
CC polynucleotides may be used to treat disorders associated with decreased  
CC expression or activity of NOVX by supplementing the patient our  
CC production or to rectify mutations. Conversely, antisense NA molecules  
CC binding with the cells own genes and preventing their expression. NOVX  
CC polynucleotides and complementary sequences may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar sequences in samples, and so which patients may be in need of  
CC restorative therapy. NOVX polypeptides may also be used as antigens in  
CC the production of antibodies and in assays to identify modulators  
CC (agonists and antagonists) of the expression and activity of NOVX. The  
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be  
CC used to modulate NOVX polynucleotide expression and activity of NOVX  
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as  
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX  
CC polypeptides and polynucleotides may be used in this way to prevent,  
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious  
CC diseases, anorexia, cancer, cancer-associated cachexia, neurodegenerative  
CC disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,  
CC haematopoietic disorders, and the various dyslipidaemias, metabolic  
CC disturbances associated with obesity, the metabolic syndrome X and  
CC wasting disorders associated with chronic diseases and various cancers.  
CC They may also be used as antibacterial agents. The present sequence  
CC represents the amino acid sequence of a human NOVX protein.

XX SQ Sequence 620 AA;

Query Match 93.8%; Score 2440; DB 8; Length 620;  
Best Local Similarity 99.6%; Pred. No. 8.1e-238;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANRSLNLFQCKPFFMTQQQMSPLREGIIDLALFVLFE 60  
DB 5 MLKFKYGARNPLDAGAAEPIANRSLNLFQCKPFFMTQQQMSPLREGIIDLALFVLFE 64  
QY 61 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
DB 65 ECSQPALMKIKHVSFNFRKYSDTIAELQELQPSAKDFEVRSLVGGCHFAEVQVREKATG 124  
QY 121 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNKHLXLYVMVEYQGG 180  
DB 125 DIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYAFQDNKHLXLYVMVEYQGG 184  
QY 181 DLLSLNRYEDQDENLQYLAELILAVHSVHLMGVHRDIPENILVDRTGHIKLVDF 240  
DB 185 DLLSLNRYEDQDENLQYLAELILAVHSVHLMGVHRDIPENILVDRTGHIKLVDF 244  
QY 241 GSAAKMNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGYGLDCDWSVGVIAYEMHYGR 300  
DB 245 GSAAKMNSNKNVNAKPIGTPDYMAPEVLTVMNGDGKGYGLDCDWSVGVIAYEMHYGR 304  
QY 301 SPFAEGTSARTENNNKQRFELKFPDDPKVSSDFDLIOQLLCCQERLKFEGELCCHPFF 360  
DB 305 SPFAEGTSARTENNNKQRFELKFPDDPKVSSDFDLIOQLLCCQERLKFEGELCCHPFF 364  
QY 361 SKIDWNINRSPFPFVTLKSDDDTSNFDPEKNSWSSPQSLSPGSGSGELPVGFS 420  
DB 365 SKIDWNINRSPFPFVTLKSDDDTSNFDPEKNSWSSPQSLSPGSGSGELPVGFS 424

QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKV 468  
DB 425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLIKSKELQDSQDKCHKV 472

RESULT 9  
ADAO5644  
ID ADA05644 standard; protein; 623 AA.

XX AC ADA05644;  
XX DT 06-NOV-2003 (first entry)  
XX DE Human NOV1b protein SEQ ID NO:4.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;  
KW immunomodulator; cytostatic; nootropic; neuroprotective;  
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;  
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX WO2003029424-A2.  
XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

02-OCT-2001; 2001US-0326483P.  
05-OCT-2001; 2001US-0327435P.  
05-OCT-2001; 2001US-0327449P.  
09-OCT-2001; 2001US-0327917P.  
09-OCT-2001; 2001US-0328029P.  
09-OCT-2001; 2001US-0328044P.  
09-OCT-2001; 2001US-0328056P.  
12-OCT-2001; 2001US-0328849P.  
15-OCT-2001; 2001US-0329414P.  
17-OCT-2001; 2001US-0330142P.  
18-OCT-2001; 2001US-0330309P.  
18-OCT-2001; 2001US-0341058P.  
24-OCT-2001; 2001US-039266P.  
24-OCT-2001; 2001US-0343829P.  
29-OCT-2001; 2001US-0349575P.  
01-NOV-2001; 2001US-0346357P.  
17-APR-2002; 2002US-0373260P.  
19-APR-2002; 2002US-0373815P.  
19-APR-2002; 2002US-0373817P.  
19-APR-2002; 2002US-0373826P.  
19-APR-2002; 2002US-0373884P.  
22-APR-2002; 2002US-0374977P.  
16-MAY-2002; 2002US-0381037P.  
16-MAY-2002; 2002US-0381038P.  
16-MAY-2002; 2002US-0381042P.  
17-MAY-2002; 2002US-0381642P.  
28-MAY-2002; 2002US-0383656P.  
29-MAY-2002; 2002US-0383831P.  
25-JUN-2002; 2002US-0391335P.  
01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;  
PI Ort T, Gorman L, Zehrhusen BD, Anderson DW, Zhong M, Catterton E;  
PI Shi W, Miller CE, Rastelli L, Stone DU, Pena CE, Shenoy SG;  
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;  
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;  
XX WPI: 2003-381626/36.  
DR N-PSDB; ADA05643.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,  
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,  
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
PS Claim 1; Page 100-101; 586pp; English.  
XX  
CC The present invention describes NOVX proteins, where X can be 1 to 55  
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide  
CC described above and a carrier; (2) a kit comprising, in one or more  
CC containers, the composition described above; (3) an isolated nucleic acid  
CC molecule which encodes a NOVX protein of the invention; (4) a vector  
CC comprising the nucleic acid molecule described above; (5) a cell  
CC comprising the above vector; (6) an antibody that immunospecifically  
CC binds to the polypeptide described above; (7) methods for determining the  
CC presence or amount of the above polypeptide or nucleic acid molecule in a  
CC sample; (8) methods for determining the presence of or predisposition to  
CC a disease associated with altered levels of expression of the above  
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a  
CC method of identifying an agent that binds to the polypeptide described  
CC above; (10) a method for identifying a potential therapeutic agent for  
CC use in treating a pathology that is related to an aberrant expression or  
CC aberrant physiological interactions of the polypeptide; (11) a method of  
CC screening for a modulator of activity or of latency or predisposition to  
CC a pathology associated with the polypeptide; (12) a method for modulating  
CC the activity of the polypeptide described above; (13) methods of treating  
CC or preventing a pathology associated with the above polypeptide in a  
CC mammal; and (14) a method for producing the above polypeptide. NOVX  
CC sequences have antidiabetic, anorectic, antibacterial, virucide,  
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian  
CC and antilipase activities, and can be used in gene therapy. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease. The polypeptide or the nucleic  
CC acid molecule may be used to diagnose, treat or prevent metabolic  
CC disorders such as diabetes or obesity, infections, cachexia, cancer,  
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's  
CC disease, immune disorders, haematopoietic disorders and various  
CC dyslipidaemias. The nucleic acids can also be used as hybridisation  
CC probes, in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The present sequence represents a human NOVX from the  
CC present invention.  
XX

SQ Sequence 623 AA;

Query Match 93.8%; Score 2440; DB 6; Length 623;  
Best Local Similarity 99.6%; Pred. No. 8.2e-238;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFYKARNPLDAGAAEPIANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 60  
Db 5 MLKFYKARNPLDAGAAEPIANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 64  
QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCGHFAEVQVREKATG 120  
Db 65 ECSOPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCGHFAEVQVREKATG 124  
QY 121 DIYAMVKMKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKXHLVLYMEYOPGG 180  
Db 125 DIYAMVKMKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKXHLVLYMEYOPGG 184  
QY 181 DLLSLNRYEDQDLENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGILKLVDF 240  
Db 185 DLLSLNRYEDQDLENLIQFYLAELILAVSHVLMGYVHRDIKPENILVDRTHGILKLVDF 244  
QY 241 GSAAKNSKNWNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDCDWWSGVYAYEMVYGR 300  
Db 245 GSAAKNSKNWNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDCDWWSGVYAYEMVYGR 304  
QY 301 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIQLSLCGQKERLKFEGLCCHPFF 360  
Db 305 SPFAEGTSARTFNNIMNFQRLKFPDDPKVSSDFDLIQLSLCGQKERLKFEGLCCHPFF 364

QY 361 SKIDWNIRNSPPFPVFTLKSDDDTSNDFEPEKNSWVSSPQCLSPSGSGELPVGFS 420  
Db 365 SKIDWNIRNSPPFPVFTLKSDDDTSNDFEPEKNSWVSSPQCLSPSGSGELPVGFS 424  
QY 421 YSKALGILGRSWSVGLDSPAKTSMSEKLLIKSKELQSDQKCHKV 468  
Db 425 YSKALGILGRSWSVGLDSPAKTSMSEKLLIKSKELQSDQKCHKV 472

RESULT 10

AB881928

ID ABB81928 standard; protein; 1958 AA.

XX ABB81928;

XX 10-OCT-2002 (first entry)

XX Human kinase #2.

XX Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;  
KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer.

XX Homo sapiens.

XX WO200259325-A2.

XX 01-AUG-2002.

XX 20-DEC-2001; 2001WO-US050497.

XX 27-DEC-2000; 2000US-0258335P.

XX (LEXI-) LEXICON GENETICS INC.

XX Yu X, Miranda M, Friddle CJ;

XX WPI: 2002-599796/54.

XX N-PDSB; ABQ78871.

XX Novel polynucleotide encoding human proteins that are structurally  
PT similar to animal kinases, useful for drug screening, diagnosis, in gene  
PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
PT applications.

XX Claim 4; Page 46-50; 50pp; English.

XX The invention relates to a novel human protein that shares structural  
CC similarity with animal kinases, including serine-threonine kinases,  
CC particularly Citron rho-interacting kinases. The proteins of the  
CC invention have nootropic and cytostatic activity. The polynucleotides may  
CC have a use in gene therapy. The encoded novel polypeptides are useful for  
CC generating antibodies, as reagents in diagnostic assays, for identifying  
CC other cellular gene products related to NHP and as reagents in assays for  
CC screening for compounds that are useful in the treatment of mental,  
CC biological or medical disorders and diseases including cancer. The  
CC sequence represents a novel human kinase of the invention

XX Sequence 1958 AA;

Query Match 93.8%; Score 2440; DB 5; Length 1958;

Best Local Similarity 99.6%; Pred. No. 5.4e-237;

Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFYKARNPLDAGAAEPIANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 60

Db 1 MLKFYKARNPLDAGAAEPIANRASRLNLFQKPPFMTQQQMSPLSRGILDALFVLFE 60

QY 61 ECSOPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCGHFAEVQVREKATG 120

Db 61 ECSOPALMKIKHVSNFVRKYSDTIAELQLOPSAKDFEVRSLVGCGHFAEVQVREKATG 120

QY 121 DIYAMVKMKKALLAQEQVSFFBEERNILSRSTSPWIPOLQYAFQDKXHLVLYMEYOPGG 180

Db 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
 Qy 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGVYHRDIKPENILVDRTHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGVYHRDIKPENILVDRTHIKLVDF 240  
 Qy 241 GSAAKNSKMNKVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMTYGR 300  
 Db 241 GSAAKNSKMNKVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMTYGR 300  
 Qy 301 SPFAEGTSARTFNNINWTFORFLKFPDDPKVSSDFDLILQSLCGQKRLKEEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNINWTFORFLKFPDDPKVSSDFDLILQSLCGQKRLKEEGLCCHPFF 360  
 Qy 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFEDEPEKNSWSSPCQLSPSGFSGEELPFVVGFS 420  
 Db 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFEDEPEKNSWSSPCQLSPSGFSGEELPFVVGFS 420  
 Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELODSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELODSQDKCHKM 468

RESULT 11  
 ABB81927  
 ID ABB81927 standard; protein; 2054 AA.  
 XX  
 AC ABB81927;  
 XX  
 DT 10-OCT-2002 (first entry)  
 XX  
 DE Human kinase #1.  
 XX  
 KW Human; kinase; enzyme; serine-threonine kinase; neutrotropic; cytosolic;  
 KW Citron rho-interacting kinase; gene therapy; mental disorder; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200259325-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 20-DEC-2001; 2001WO-US050497.  
 XX  
 PR 27-DEC-2000; 2000US-0258335P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Yu X, Miranda M, Friddle CJ;  
 XX  
 DR WPI; 2002-599796/64.  
 DR N-PSDB; ABQ78870.  
 XX  
 PT Novel polynucleotide encoding human proteins that are structurally  
 PT similar to animal kinases, useful for drug screening, diagnosis, in gene  
 PT therapy of disorders and diseases e.g. cancer and pharmacogenomic  
 PT applications.  
 XX  
 PS Claim 2; Page 39-43; 50pp; English.  
 XX  
 CC The invention relates to a novel human protein that shares structural  
 CC similarity with animal kinases, including serine-threonine kinases,  
 CC particularly Citron rho-interacting kinases. The proteins of the  
 CC invention have neutrotropic and cytosolic activity. The polynucleotides may  
 CC have a use in gene therapy. The encoded novel polypeptides are useful for  
 CC generating antibodies, as reagents in diagnostic assays, for identifying  
 CC other cellular gene products related to NHP and as reagents in assays for  
 CC screening for compounds that are useful in the treatment of mental,  
 CC biological or medical disorders and diseases including cancer. The  
 CC sequence represents a novel human kinase of the invention  
 XX  
 SQ Sequence 2054 AA;

Query Match 93.8%; Score 2440; DB 5; Length 2054;  
 Best Local Similarity 99.6%; Pred. No. 5.8e-237;  
 Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDAGAAEPIANRAGRLNLFQGGKPPFMTQQQMSPLSREGILDALVLF 60  
 Db 1 MLKFKYGARNPLDAGAAEPIASRSLNLFQGGKPPFMTQQQMSPLSREGILDALVLF 60  
 Qy 61 ECSQPALMKIKHVSFVRKYSDTIAELQLOPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDTIAELQLOPSAKDFEVRSLVGGCHFAEVQVREKATG 120  
 Qy 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
 Db 121 DIYAMKVMKKALLAQEQVSEFEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQPGG 180  
 Qy 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGVYHRDIKPENILVDRTHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLQFYLAELILAVHSVHLMGVYHRDIKPENILVDRTHIKLVDF 240  
 Qy 241 GSAAKNSKMNKVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMTYGR 300  
 Db 241 GSAAKNSKMNKVNAKLPICGTPDYMAPEVLTVMNGDGKGTGYGLDCDMSVGVYAYEMTYGR 300  
 Qy 301 SPFAEGTSARTFNNINWTFORFLKFPDDPKVSSDFDLILQSLCGQKRLKEEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNNINWTFORFLKFPDDPKVSSDFDLILQSLCGQKRLKEEGLCCHPFF 360  
 Qy 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFEDEPEKNSWSSPCQLSPSGFSGEELPFVVGFS 420  
 Db 361 SKIDWNINRNSPPFPVPTLKSDDDTSNFEDEPEKNSWSSPCQLSPSGFSGEELPFVVGFS 420  
 Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELODSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELODSQDKCHKM 468

RESULT 12  
 AAE24150  
 ID AAE24150 standard; protein; 2054 AA.  
 XX  
 AC AAE24150;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human kinase (PKIN)-21 protein.  
 XX  
 KW Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;  
 KW acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;  
 KW asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;  
 KW development; hepatitis; cardiovascular; hypertension; drug screening;  
 KW myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;  
 KW fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;  
 KW hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hiv;  
 KW neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;  
 KW hyperlipidaemia; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 97..360  
 FT Domain /note= "Eukaryotic protein kinase domain"  
 FT Domain 98..241  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 99..349  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 101..241  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 102..241  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 249..349  
 FT Domain /note= "Protein kinase domain"  
 FT Domain 258..445



FT Domain /note= "Protein kinase domain"  
FT 258..349  
FT /note= "Protein kinase domain"  
FT 534..542  
FT /note= "Domain found in NIK1-like kinase"  
FT 854..875  
FT /note= "Leucine zipper pattern"  
FT 891..933  
FT /note= "Domain found in NIK1-like kinase"  
FT 964..975  
FT /note= "Domain found in NIK1-like kinase"  
FT 991..1012  
FT /note= "Leucine zipper pattern"  
FT 1015..1067  
FT /note= "Domain found in NIK1-like kinase"  
FT 1057..1078  
FT /note= "Leucine zipper pattern"  
FT 1159..1180  
FT /note= "Leucine zipper pattern"  
FT 1217..1255  
FT /note= "Domain found in NIK1-like kinase"  
FT 1388..1434  
FT /note= "Domain found in NIK1-like kinase"  
FT 1390..1438  
FT /note= "Phorbol esters/diacylglycerol binding site"  
FT 1403..1466  
FT /note= "Phorbol esters/diacylglycerol binding site"  
FT 1471..1590  
FT /note= "PH domain"  
FT 1619..1916  
FT /note= "CNH domain"  
FT 1759..1802  
FT /note= "Domain found in NIK1-like kinase"  
FT 1819..1831  
FT /note= "Domain found in NIK1-like kinase"  
FT 1851..1880  
FT /note= "Domain found in NIK1-like kinase"  
XX  
XX WO200233099-A2.  
XX  
XX 25-APR-2002.  
XX  
XX 20-OCT-2001; 2001WO-US047728.  
XX  
XX 20-OCT-2000; 2000US-0242410P.  
XX 27-OCT-2000; 2000US-0240568P.  
XX 03-NOV-2000; 2000US-0245708P.  
XX 09-NOV-2000; 2000US-0247672P.  
XX 16-NOV-2000; 2000US-0249565P.  
XX 22-NOV-2000; 2000US-0252730P.  
XX 01-DEC-2000; 2000US-0250807P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;  
PI Gao MG, Ramkumar J, Ding L, Tang Y, Hafalia AJA, Nguyen DB;  
PI Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;  
PI Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;  
PI Thangavelu K, Khan PA, Ison CH;  
XX  
XX WPI: 2002-454603/48.  
XX N-PSDB: AAD38864.  
XX  
XX New human kinase polypeptide, for diagnosing, preventing and treating  
XX cancer, immune system disorders, growth and development disorders,  
XX cardiovascular disorders and lipid disorders.  
XX  
XX Claim 1; Page 177-182; 210pp; English.  
XX  
XX The invention relates human kinases (PKIN) and their corresponding  
XX nucleic acid sequences. PKIN and its DNA are useful for diagnosing,  
XX treating and preventing cancer, an immune system disorder (e.g., acquired  
XX immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,

CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting  
CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),  
CC cardiovascular disorder (e.g., hypertension, myocardial infarction,  
CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,  
CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,  
CC hyperlipidaemia, obesity), and for assessing the effects of exogenous  
CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a  
CC condition or a disease associated with the expression of PKIN in a  
CC biological sample. A composition comprising PKIN or an agonist or  
CC antagonist of PKIN is useful for treating a disease or condition  
CC associated with decreased or increased expression of functional PKIN.  
CC PKIN is useful in a number of drug screening techniques and to analyse  
CC the proteome of a tissue or cell type. PKIN DNA is useful for creating  
CC knockin humanised animals or transgenic animals to model human diseases,  
CC and in somatic or germline gene therapy. The present sequence is human  
XX PKIN protein  
XX  
XX SQ Sequence 2054 AA;  
Query Match 93.8%; Score 2440; DB 5; Length 2054;  
Best Local Similarity 99.6%; Pred. No. 5,8e-237;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLKFKYGARNPIDAGAAEPIANRASRLNLPFGQKPPFTQOMSPLSREGILDALFVLFE 60  
DB 1 MLKFKYGARNPIDAGAAEPIASRASRLNLPFGQKPPFTQOMSPLSREGILDALFVLFE 60  
QY 61 ECSQPALMKIKHVSNFVRKYSDDTIAELOQPSAKDFEVRSLVCGHFAEVQVVRKATG 120  
DB 61 ECSQPALMKIKHVSNFVRKYSDDTIAELOQPSAKDFEVRSLVCGHFAEVQVVRKATG 120  
QY 121 DIYAMKVMKKVALLAQEQVSFFEBERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
DB 121 DIYAMKVMKKVALLAQEQVSFFEBERNILSRSTSPWIPQLQYAFQDKNHLVLMVEYQPGG 180  
QY 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVYVHRDIKPNILVDRTHIKLVDF 240  
DB 181 DLLSLNRYEDQDENLIQFYLAELILAVHSVHLMGVYVHRDIKPNILVDRTHIKLVDF 240  
QY 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMLYGR 300  
DB 241 GSAAKMNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKGTGLDCDWSVGVIAEMLYGR 300  
QY 301 SPFAEGTSARTFNIMNFQRLKFPDDPKVSSDFLDLIQSLCCQKRLKPEGLCCHPFF 360  
DB 301 SPFAEGTSARTFNIMNFQRLKFPDDPKVSSDFLDLIQSLCCQKRLKPEGLCCHPFF 360  
QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCQLSPSGFGEELPFVGFPS 420  
DB 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWVSSPCQLSPSGFGEELPFVGFPS 420  
QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
DB 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQSDQKCHKV 468  
RESULT 13  
AAO26959  
ID AAO26959 standard; protein; 2054 AA.  
XX AC AAO26959;  
XX AC AAO26959;  
XX  
XX 01-MAY-2003 (first entry)  
XX Human CRK protein sequence, SEQ ID No 2.  
XX  
XX Anorectic; hypotensive; cardiant; antilipaeamic; cerebroprotective;  
XX antitumor; osteopathic; antiarthritic; cytostatic; antidepressant;  
XX immunomodulator; antitumor; tranquiliser; antiparkinsonian; nootropic;  
XX neuroprotective; antiinflammatory; antidiabetic; analgesic;  
XX human ciron rho/rac-interacting kinase; enzyme; CRK; ameliorating;  
XX obesity; comorbidity; cancer; anorexia; cachexia; bulimia;  
XX central nervous system disorder; chronic obstructive pulmonary disease;

diabetes; pain.  
Homo sapiens.  
WO2003004523-A1.  
16-JAN-2003.  
28-JUN-2002; 2002WO-EP007156.  
02-JUL-2001; 2001US-0301841P.  
11-DEC-2001; 2001US-0338651P.  
25-APR-2002; 2002US-0375014P.  
(FARB ) BAYER AG.  
Zhu Z;  
WPI; 2003-221576/21.  
N-PSDB; AAL55214.  
New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or Alzheimer's disease.  
Claim 1; Fig 2; 237pp; English.  
The invention relates to an isolated polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer), anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's disease), chronic obstructive pulmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polynucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This sequence represents the human CRIK protein of the invention

Query Match 93.8%; Score 2440; DB 6; Length 2054;  
Best Local Similarity 99.6%; Pred. No. 5.8e-237;  
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNPLDAGAAEPIANPASRLNLFQCKPPFTQQQMSPLSRGILDALFVLE 60  
DB 1 MLKFKYGARNPLDAGAAEPIASASRLNLFQCKPPFTQQQMSPLSRGILDALFVLE 60  
QY 61 ECSQPALMKIKHVSFVRKYSYDTIAELOQLPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
DB 61 ECSQPALMKIKHVSFVRKYSYDTIAELOQLPSAKDFEVRSLVGCCHFAEVQVREKATG 120  
QY 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQAFQDNHLYLVMEYQPG 180  
DB 121 DIYAMKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQAFQDNHLYLVMEYQPG 180  
QY 181 DILSLNRYEQDQDENLIQFYLAELILAVSHVLMGVYVHRDKPENILVDRTHGKLVDF 240  
DB 181 DILSLNRYEQDQDENLIQFYLAELILAVSHVLMGVYVHRDKPENILVDRTHGKLVDF 240

QY 241 GSAAKNSNKNVNAKLPICTPDYMAPEVLTVNNGDKGKTYGLDCDWWSVGVYAYEMIYGR 300  
DB 241 GSAAKNSNKNVNAKLPICTPDYMAPEVLTVNNGDKGKTYGLDCDWWSVGVYAYEMIYGR 300  
QY 301 SPFAEGTSARTNNINNFQRLKFPDDPKVSSDFLDLIQSLCCGOKERLKPEGLCCHPFF 360  
DB 301 SPFAEGTSARTNNINNFQRLKFPDDPKVSSDFLDLIQSLCCGOKERLKPEGLCCHPFF 360  
QY 361 SKIDMNNIENSPPPFVFTLKSDDDTSNFDPEPKNGWVSSPCQLSPSGFSGBELFVGFS 420  
DB 361 SKIDMNNIENSPPPFVFTLKSDDDTSNFDPEPKNGWVSSPCQLSPSGFSGBELFVGFS 420  
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKXKLIKSKELQDSODKCHKV 468  
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKXKLIKSKELQDSODKCHKV 468

RESULT 14  
AAE24079  
ID AAE24079 standard; protein; 2053 AA.  
XX  
AAE24079;  
AC  
XX  
DT 04-OCT-2002 (first entry)  
XX  
XX Human MDPK protein.  
XX  
KW Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein; tumourigenesis; tumour growth; tumour metastasis; viral infection; skeletal muscle disorder; muscular dystrophy; myotonic dystrophy; immune disorder; neoplastic disorder; gene therapy.  
OS Homo sapiens.  
FH Key  
Domain 53..303 /note= "pkinase domain"  
Domain 97..360 /note= "pkinase domain"  
Region 195..210 /note= "Antigenic epitope"  
Region 217..229 /note= "Serine/Threonine protein kinase active site signature"  
Region 455..475 /note= "Antigenic epitope"  
Domain 1588..1865 /note= "CNH domain"  
XX  
PN WO200234896-A2.  
XX  
XX 02-MAY-2002.  
XX  
PF 23-OCT-2001; 2001WO-US050636.  
XX  
PR 23-OCT-2000; 2000US-0242429P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Kapeller-Libermann R;  
PI  
DR WPI; 2002-479720/51.  
XX N-PSDB; AAD39191.  
XX  
PT Human myotonic dystrophy type protein kinase polypeptide and polynucleotide useful for prognosticating, diagnosing, preventing or inhibiting tumorigenesis, tumor growth, tumor metastasis and viral infection.  
PS Claim 8; Fig 3; 148pp; English.  
XX  
CC The invention relates to human myotonic dystrophy type protein kinase

CC (MDPK) polypeptides designated as 13245 and nucleic acid molecules  
 CC encoding such polypeptides. 13245 molecules are used to develop  
 CC diagnostic and therapeutic agents for prognosticating, diagnosing,  
 CC preventing, inhibiting, alleviating or curing MDPK-related disorders.  
 CC Polypeptides of the invention are used to develop diagnostic and  
 CC therapeutic agents for 13245-mediated or related disorders such as  
 CC tumorigenesis, tumour growth, tumour metastasis, viral infection of a  
 CC cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),  
 CC immune disorders and neoplastic disorders. The invention is also used in  
 CC gene therapy. The present sequence is human MDPK protein  
 XX  
 XX Sequence 2053 AA;

Query Match 93.4%; Score 2430; DB 5; Length 2053;  
 Best Local Similarity 99.1%; Pred. No. 6e-236;  
 Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGPPMTQQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGPPMTQQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 QY 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQOYAFQDKNHLVLMVEYOPGG 180  
 Db 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQOYAFQDKNHLVLMVEYOPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDMSVGVIAEMIIYGR 300  
 Db 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDMSVGVIAEMIIYGR 300  
 QY 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFDLIIQSLGQKERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFDLIIQSLGQKERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468

RESULT 15  
 ADF60994  
 ID ADF60994 standard; protein; 2053 AA.  
 XX  
 AC ADF60994;  
 XX

DT 12-FEB-2004 (first entry)  
 XX  
 DE Pain associated human 2207 polypeptide.  
 DE

XX Pain modulation; pain disorder; painful disorder; potassium channel;  
 KW kinase expression; inflammatory pain; chronic pain; neuropathic pain;  
 KW causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain;  
 KW analgesic; antiinflammatory.

XX Homo sapiens.  
 XX  
 XX US2003153525-A1.  
 XX  
 XX 14-AUG-2003.  
 XX  
 XX 19-DEC-2002; 2002US-00325430.  
 XX

PR 19-DEC-2001; 2001US-0341953P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Silos-Santiago I, Rosenfeld JB,  
 PI  
 XX WPI; 2003-897732/82.  
 DR N-PSDB; ADF60992, ADF60993.  
 XX  
 PT Identifying a compound capable of treating a pain disorder comprises  
 PT assaying the ability of the compound to modulate specific, e.g., kinases  
 PT or potassium channel, nucleic acid expression or polypeptide activities.  
 XX  
 XX Disclosure; SEQ ID NO 12; 80pp; English.  
 PS  
 XX The present invention relates to a method for identifying a compound  
 CC capable of modulating pain or painful disorders. The method comprises  
 CC assaying the ability of the compound to modulate specific nucleic acid  
 CC expression or polypeptide activity e.g. potassium channel, or kinase  
 CC expression/activity. The method and compounds are useful for treating  
 CC pain or painful disorders e.g. inflammatory pain, chronic pain,  
 CC neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache  
 CC pain and tissue pain. The present sequence represents a human protein  
 CC associated with pain.  
 XX  
 SQ Sequence 2053 AA;

Query Match 93.4%; Score 2430; DB 7; Length 2053;  
 Best Local Similarity 99.1%; Pred. No. 6e-236;  
 Matches 464; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGPPMTQQQMSPLSREGILDALFVLFE 60  
 Db 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFQGGPPMTQQQMSPLSREGILDALFVLFE 60  
 QY 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 Db 61 ECSQPALMKIKHVSFVRKYSDDTIAELQELQPSAKDFEVSRLVCGGHFAEVQVVRKATG 120  
 QY 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQOYAFQDKNHLVLMVEYOPGG 180  
 Db 121 DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQOYAFQDKNHLVLMVEYOPGG 180  
 QY 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 Db 181 DLLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKPNILVDRTGHIKLVDF 240  
 QY 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDMSVGVIAEMIIYGR 300  
 Db 241 GSAAKMNSKNVNAKLPIGTPDYMAPEVLTVMNGDGKGTGGLDCDMSVGVIAEMIIYGR 300  
 QY 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFDLIIQSLGQKERLKFEGLCCHPFF 360  
 Db 301 SPFAEGTSARTFNINMFORFLKPPDDPKVSSDFDLIIQSLGQKERLKFEGLCCHPFF 360  
 QY 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
 Db 361 SKIDWNIRNSPPFPVPTLKSDDDTSNFDEPEKNSWSSPCQLSPSGSGEELPFVGF 420  
 QY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468  
 Db 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV 468

Search completed: November 8, 2004, 12:28:13  
 Job time : 160 secs

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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 04:16:56 ; Search time 4438 Seconds  
(without alignments)  
12439.431 Million cell updates/sec

Title: US-10-724-594-1  
Perfect score: 1515  
Sequence: 1 999gagatgttgaaagttcaa.....tctgagcgcgtgacgta 1515

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	602.6	39.8	698	5	BP146990
2	521.2	34.4	1085	4	BM904785
3	452.8	29.9	600	4	EG808136
4	423.8	28.0	427	4	EG944539
5	413.2	27.3	617	5	BQ417810
6	380	25.1	481	7	CN682405
7	378	25.0	479	7	CN678533
8	351.4	23.2	490	2	BF562826
9	344.2	22.7	821	4	BI454262
10	329.2	21.7	450	9	CG501400
11	328.8	21.7	423	2	BF344814
12	327	21.6	449	9	CG501399
13	318.2	21.0	512	9	CG652891
14	314.2	20.7	340	2	BF380737
15	312.6	20.6	582	5	BX516231
16	281.6	18.6	521	1	AI882189
17	281.4	18.6	355	8	CC325092
18	278.8	18.4	539	2	AW525215
19	276.4	18.2	325	3	BC008127
20	272.8	18.0	336	9	CG869028
21	270.8	17.9	321	2	BF932611
22	262.4	17.3	335	2	BF763211
23	262.4	17.3	524	7	CK841805
24	251.8	16.6	423	2	BB827314

25	251.4	16.6	398	5	BY018641
26	246.2	16.3	385	9	CG555761
27	246.2	16.3	289	6	BF944809
28	246	16.2	508	6	CB783081
29	245.8	16.2	547	7	CF744826
30	245.8	16.2	647	7	CF744826
31	244.8	16.2	801	5	BU475240
32	244.8	16.2	847	5	BU467302
33	243.4	16.1	907	7	CK147448
34	240.8	15.9	401	5	BY602044
35	238.8	15.8	2688	3	BC024150
36	237.2	15.7	2862	3	BC056615
37	236	15.6	1478	9	AY408842
38	233.6	15.4	605	5	BP168081
39	233.4	15.4	563	6	CD310916
40	231.6	15.3	370	5	BY021399
41	231.4	15.3	423	2	BB823725
42	225.2	14.9	1600	3	BC038993
43	222	14.7	400	1	AL360718
44	219.4	14.5	525	2	BF558465
45	218.4	14.4	1472	9	AY408840

ALIGNMENTS

RESULT 1  
LOCUS BP146990 698 bp mRNA linear EST 30-DEC-2003  
DEFINITION BP146990 full-length enriched swine cDNA library, adult ovary Sus  
ACCESSION BP146990  
VERSION BP146990.1 GI:40396461  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,  
Okumura, N., Hamasima, N. and Awata, T.  
TITLE PEST (Pig EST Data Explorer): construction of a database for ESTs  
JOURNAL derived from porcine full-length cDNA libraries  
COMMENT Nucleic Acids Res. 32 (1), D484-D488 (2004)  
Contact: Hirohide Uenishi  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STAFF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

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/clone="OVRM10025B09"  
/tissue\_type="ovary"  
/dev stage="adult"  
/clone\_lib="full-length enriched swine cDNA library, adult  
ovary"  
Query Match 39.8%; Score 602.6; DB 5; Length 698;  
Best Local Similarity 91.4%; Pred. No. 2.8e-172;



REFERENCE 1 (bases 1 to 600)  
 AUTHORS Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.  
 TITLE Gene expression in the developing mouse retina by EST sequencing and microarray analysis  
 JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)  
 MEDLINE 21671825  
 PUBMED 11812828  
 COMMENT Contact: Klein WH  
 Department of Biochemistry and Molecular Biology  
 University of Texas M.D. Anderson Cancer Center  
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
 Tel: 713 792 3646  
 Fax: 713 790 0329.

FEATURES Location/Qualifiers  
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ORIGIN  
 Query Match 29.9%; Score 452.8; DB 4; Length 600;  
 Best Local Similarity 86.6%; Pred. No. 1.8e-126;  
 Matches 499; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1 GGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCTTTGGATGCTGTGCTGAA 60  
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 QY 61 CCCATTGCCAACCGGCTCCAGCTGAATCTCTTCTCCAGGGGAACACCCCTTATG 120  
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 QY 121 ACTCAACAGCAGATGTCCTCTTCTCCGAGAGGAGATATAGATGCCCTCTTTGTCTC 180  
 DB 145 ACTCAACAGCAGATGTCCTCTTCTCCGAGAGGAGATGTCAGACGCCCTCTTCGCTCTC 204  
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 DB 265 AAGTATTCACACCACTAGCCAGTTCGCGAGCTCGAGCCCTCGCGAGAGACTTCGAA 324  
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 DB 325 GTTCGAAGCTTTGTGGCTGTGTCACCTTCGCTGAAGTGCAGGTGTTAGAGAAAGGG 384  
 QY 361 ACCGGGACATCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 DB 385 ACCGGGAGCTCTATGCTATGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444  
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 QY 541 GGAGGGGACTTGTGTCTCTTTTGAATAGATAGAG 576  
 DB 565 GGAGGGGATTTGTCTGCTTCTGACAGATACGAG 600

RESULT 4  
 BG944539  
 LOCUS  
 DEFINITION ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library) EST 15-JAN-2003

Homo sapiens cDNA clone ax51f11 random, mRNA sequence.  
 BG944539  
 VERSION BG944539.1 GI:14343911  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.  
 Gene expression in proliferating human erythroid cells  
 Genomics 59 (2), 168-177 (1999)  
 99339981  
 MEDLINE 10409428  
 PUBMED  
 COMMENT Contact: Jeffery L. Miller  
 Laboratory of Chemical Biology  
 National Institute of Diabetes and Digestive and Kidney Diseases  
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA  
 Tel: 301 402 2373  
 Fax: 301 435 5148  
 Email: jmf@nih.gov  
 DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).  
 Plate: 51 row: f column: 11  
 Seq primer: -21M13 forward primer (ABI).  
 Location/Qualifiers  
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 /clone="ax51f11"  
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 /cell\_line="Primary Culture of Peripheral Blood Mononuclear Cells"  
 /dev\_stage="Progenitor; EPO responsive CD71++++"  
 /lab\_host="SOLR"  
 /clone\_lib="Hembase; Erythroid Progenitor Cells (LCB:ax library)"  
 /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: EcoRI; 65,000 proliferating erythroid cells from the Buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."

ORIGIN  
 Query Match 28.0%; Score 423.8; DB 4; Length 427;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-117;  
 Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 148 CGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATCAGTCAGCTGCTCTG 207  
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 QY 208 ATGAAGATTAGACGCTGAGCACTTTGTCGGAAGTATTCGACACCATAGCTGAGTTA 267  
 DB 61 ATGAAGATTAGACGCTGAGCACTTTGTCGGAAGTATTCGACACCATAGCTGAGTTA 120  
 QY 268 CAGGAGCTCCAGCTTCGGCAAGAGACTTCGAAGTCAGAAGTCTTTGAGTTGGTTCAC 327  
 DB 121 CAGGAGCTCCAGCTTCGGCAAGAGACTTCGAAGTCAGAAGTCTTTGAGTTGGTTCAC 180

QY 328 TTGTGCTGAAGTCAAGTGTATAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGTG 387  
 Db 181 TTGTGCTGAAGTCAAGTGTATAGAGAGAAAGCAACCGGGGACATCTATGCTATGAAGTG 240  
 QY 388 ATGAAGAAGAGGCTTTATTGGCCCGAGGAGGAGTTTCAATTTTGGAGGAAGCGGAAC 447  
 Db 241 ATGAAGAAGAGGCTTTATTGGCCCGAGGAGGAGTTTCAATTTTGGAGGAAGCGGAAC 300  
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 Db 301 ATATTATCTCGAGTACAAAGCCCGGATCCCGCAATACAGTATGCTTTTCAGACAAA 360  
 QY 508 AATCACTTTATCTGTGTCATGGAATATCAGCTCGAGGGGACTTCTGCTCACTTTTGAAT 567  
 Db 361 AATCACTTTATCTGTGTCATGGAATATCAGCTCGAGGGGACTTCTGCTCACTTTTGAAT 420  
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 Db 421 AGATATG 427

RESULT 5  
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 LOCUS  
 DEFINITION BQ417810.1 617 bp mRNA linear EST 23-MAY-2002  
 1k51b06.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to  
 TR:088937 088937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.  
 ; mRNA sequence.

ACCESSION BQ417810  
 VERSION BQ417810.1 GI:21123011  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 617)  
 AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
 Lemshka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bliscain, A.,  
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,  
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,  
 Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138

Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Pancreas was obtained from Gerard Gradwohl (PNAS 97 p1607-1611,  
 2000) Library was constructed by Catherine Lee DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Marie Searce  
 (msearce@mail.med.upenn.edu)

Seq primer: -40RP from Gibco  
 High quality sequence stop: 367.  
 Location/Qualifiers  
 1. .617

FEATURES  
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/organism="Mus musculus"  
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 /note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site\_1:  
 Not 1; Site 2: Sal I; The library was prepared by  
 Catherine S. Lee and has not been published. The pancreas  
 was obtained from Gerard Gradwohl (PNAS 97 p1607-1611,  
 2000). The cDNA's were prepared with an oligo containing a

NotI site, and SalI linkers were added to the ends. The  
 inserts were cut with NotI before being cloned into the  
 NotI-SalI sites in the vectors. This is one of two  
 libraries, ngn3 wt and ngn3 -/-. The wt library is in  
 pSPORT1, T7 promoter is 5'.

ORIGIN  
 Query Match 27.3%; Score 413.2; DB 5; Length 617;  
 Best Local Similarity 86.1%; Pred. No. 2.3e-114;  
 Matches 457; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
 QY 1 GGGAGATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTGGATGCTGGTCTGTGAA 60  
 Db 87 GGAAGATGTTGAAGTTCAAATATGAGCGCGGAATCCCTTGGATGCTGGTCTGTGAA 146  
 QY 61 CCCATTGCCAACCGGGCTCCAGGCTGAATCTCTTCCAGGGGAAACACCCCTTTATG 120  
 Db 147 CCCATTGCCAGTCGGGCTCCAGGCTGAATCTCTTCCAGGGGAAACCGCCCTCATG 206  
 QY 121 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 180  
 Db 207 ACTCAACAGCAGATGCTCTCTTTCCGAGAGAGGATATAGATGCCCTCTTTGTTCTC 266  
 QY 181 TTTGAAGATGCAAGTCAGCTGCTCTGATGAAGATTAAGCACTGAGCAACTTTGTCGG 240  
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 QY 361 ACCGGGACATCTATGCTATGAAGTGCATGAAGAAGAGGCTTTATTGGCCCGAGGACAG 420  
 Db 447 ACCGGGACATCTATGCTATGAAGTGCATGAAGAAGAGGCTTTATTGGCCCGAGGACAG 506  
 QY 421 GTTTCATTTTTCAGAGAGCGGACATATATTCGAGACACAGCCGTTGGATCCCC 480  
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RESULT 6

CN682405

LOCUS

DEFINITION

EO164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low

density) cDNA library (Long) Mus musculus cDNA clone NIA:EO164B04

IMAGE:30782511 5', mRNA sequence.

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 481)

REFERENCE

AUTHORS

Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,

VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C.,

Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L.,

Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,

Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,

Schlessinger, D., Keller, J., Klotz, E., Kelsey, G., Umezawa, A.,

Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,

D'Urso, M., Kelsey, J., Hide, W. and Ko, M.S.

Transcriptome analysis of mouse stem cells and early embryos

PLOS Biol. 1 (3), 410-419 (2003)

CONTACT: Dawood B. Dudekula



Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: E0164 row: B column: 04  
Seq primer: M13 Reverse  
High quality sequence stop: 481  
POLYA=No.

FEATURES  
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1. 481  
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/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long)"  
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. ES cells were plated at density 3x103/cm2, on gelatin-coated plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen]: 5'-pGACTGTTCTGATCGAGCGCGCCCTTTT-3' from 2ug of total RNA, treated with R4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.8 kb. The library was constructed by Yulan Piao."

ORIGIN  
Query Match 25.1%; Score 380; DB 7; Length 481;  
Best Local Similarity 88.0%; Pred. No. 3.1e-104;  
Matches 426; Conservative 0; Mismatches 55; Indels 3; Gaps 1;  
QY 297 CGAAGTCAGAGTCTTGTAGTGTGCTACTTTGCTGAAGTCAGCGGTGTAAGAGAA 356  
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QY 357 AGCAACCGGGACATCTATCTATGAAGTGATGAAGAGAGCGCTTTATTTGCCCCAGGA 416  
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QY 477 CCCCCATTACAGTATCCCTTCAGGACAAATACCTTTACTCTGTCATGGAATATCA 536  
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QY 657 CGTCATCGAGACATCAAGCTGAGAACATCTCGTTGACCGACACAGACACATCAAGCT 716  
Db 361 TGTGATCGAGACATCAAGCCGAGAACATCTCTCATCCGCGGAGGACACATCAAGCT 420  
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QY 777 GATT 780  
Db 478 CATT 481

RESULT 7  
CN678533  
LOCUS  
DEFINITION  
E0112C12-5 NTA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0112C12 IMAGE:30777539 5', mRNA sequence.  
ACCESSION  
CN678533  
VERSION  
EST.578533.1 GI:47444984  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
Mus musculus  
ORGANISM  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 479)  
AUTHORS  
Sharov, A.Y., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Wang, Y., Carlier, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelse, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.  
Transcriptome analysis of mouse stem cells and early embryos  
FLOS Biol. 1 (3), 410-419 (2003)  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: E0112 row: C column: 12  
Seq primer: M13 Reverse  
High quality sequence stop: 479  
POLYA=No.

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Location/Qualifiers  
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/cell\_line="129.3 ES cells"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long)"  
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. ES cells were plated at density 3x103/cm2, on gelatin-coated

plates and cultured for 48 hrs at 37 °C, 5% CO<sub>2</sub>. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-pGACTAGTTCAGATCGGAGCGCGCCCTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.8 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 25.0%; Score 378; DB 7; Length 479;  
Best Local Similarity 88.0%; Pred. No. 1.2e-103;  
Matches 424; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

```

QY 297 CGAAGTCAGAAGCTTTGTAGTTGTGGTCACTTTCTGAAAGTCAGGTTGTAAGAGAA 356
DB 1 CGAAGTTCGAAGCTTTGTGGTGTGGTCACTTTCTGAAAGTCAGGTTGTAAGAGAA 60
QY 357 ASCRACCGGGGACATCTATGCTATGAAGTGATGAAGAGAGGCTTTATTGGCCAGGA 416
DB 61 GCGACCGGGGACGCTATGCCATGAATATCATGAAGAGAGGCTTTGCTGGCCAGGA 120
QY 417 GCAGGTTTCATTTTGTAGGAAGAGCGGAACATATTCTCGAAGCACAAGCCGCTGGAT 476
DB 121 ACAGGTTTCATTTTGTAGGAAGAGGAGGACATATTCTCGGACGACAGTCTTGGAT 180
QY 477 CCCCCAATACAGTATGCTTTTCAGGACAAAATCACTTTATCTGTGTCATGGAATATCA 536
DB 181 CCCCCAGTTACAGTATGCTTTTCAGGACAAAATCACTTTATCTGTGTCATGGAATATCA 240
QY 537 GCCTGAGGGGACTTGTGCTACTTTGAATAGATATGAGGACAGATTTAGATGAACCT 596
DB 241 GCCTGAGGGGATTTGCTGTCTCTCTGACAGATACGAGGACCAATTAGATGAGCAT 300
QY 597 GATACAGTTTACCTAGTGTAGTCTGATTTGGCTGTTTCCAGCGTTTCACTGTATGGGATA 656
DB 301 GATCCAGTTTACCTTGTGCTGAGTCTGATTTGGCTGTCCACAGCGTGCCAGATGGGATA 360
QY 657 CGTGATCGAGACATCAAGCCTGAGAACATTTCTGTTGACCGCACAGGACACATCAAGCT 716
DB 361 TGTGATCGAGACATCAAGCCGAGAACATCTCATCGCCGACGGGACACATCAAGCT 420
QY 717 GGTGATTTGGATCTGCGCGGAAATGAATTCAAACAAGATGGTGAATGCCAACTCCC 776
DB 421 GGTGATTTGGATCGAGCGGCTAAGATGAATTCAAATAA---GGTGGATGCCAACTCCC 477
QY 777 GA 778
DB 478 CA 479

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## RESULT 8

BF562826  
LOCUS 490 bp mRNA linear EST 12-DEC-2000  
DEFINITION UI-R-BJ0p-aip-b-06-0-UI.r1 UI-R-BJ0p Rattus norvegicus cDNA clone  
ACCESSION BF562826  
VERSION BF562826.1 GI:11672556  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

1 (bases 1 to 490)

## AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

## TITLE

Normalization and subtraction: two approaches to facilitate gene

## JOURNAL

discovery

## MEDLINE

97044477

## COMMENT

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LiNL (info@image.llnl.gov). IMAGE ID= 1797673

Seq primer: M13 Forward

Location/Qualifiers

1..490

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BJ0p-aip-b-06-0-UI"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="UI-R-BJ0p"

/notes="Vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ0p

library is a subtracted library derived from the UI-R-AA1,

UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AE1, UI-R-AF1, and

UI-R-AG1 libraries. These libraries represent tissues from

rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal

at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV

canal at 15 dpc, and ventricle at 13 dpc. The tag is a

string of 5-6 nucleotides present between the Not I site

and the oligo-dT track. The library was constructed as

described by Bonaldo, Lennon and Soares, Genome Research

6: 791-806, 1996."

Query Match 23.2%; Score 351.4; DB 2; Length 490;

Best Local Similarity 85.6%; Pred. No. 1.7e-95;

Matches 391; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 GGGGAGATGTTGAAGTTCAAATATGAGCGCGGATCTTTGGATGCTGTCTCTGAA 60

DB 34 GGAGAGATGTTGAAGTTCAAAGTTCAGGATGAGTGCAGAACCCGTCGAGCGCCCGAG 93

QY 61 CCATTGCCAACCGGCTCCAGGCTGAATCTGTTCTTCCAGGGAAACACCCCTTTATG 120

DB 94 CCATTGCCAGTCGGGCTCCAGGCTAAATCTTCTTCCAGGGAAACCCGCTCATG 153

QY 121 ACTCAACAGCAGATGTCCTCTTTCCCGAGAAGGATATTAGATGCCCTCTTTCTTC 180

DB 154 ACTCAACAGCAGATGTCCTCTTTCCCGGGAAGGGTGTAGATGCCCTCTTTCTTC 213

QY 181 TTGAGAGATGAGTCAGCTGCTCTGATGAGATTAGACGTCGAGCAACTTGTCCGG 240

DB 214 TTGAGAGATGAGTCAGCTGCTCTGATGAGATTAGACGTCGAGCAACTTGTCCGG 273

QY 241 AAGTATTCGACACCATAGCTGAGTTACAGAGCTCCAGGCTTCGCGAAAGACTTCGAA 300

DB 274 AAGTATTCGACACCATAGCTGAGTTACAGGAGCTCCAGGCTTCGCGAAAGACTTCGAA 333

QY 301 GTCAAGATCTTGTAGTGTGCTGCTCTTCTGAGTGCAGGCTGTAAGAGAGAAACA 360

DB 334 GTGGAAGTCTTGTGGGCTGCGGTCACTTCGCGGAAGTGCAGGCTGTAGAGAGAAGGCC 393

QY 361 ACCGGGACATCTATGCTAAAGTGTGAAGAGAGCGCTTTATTGGCCCGAGGAGCAG 420  
 Db 394 ACCGGGAGTGTCTACGCCATGAAGATCATGAAGAGGCGCTTTCCGGCCCGAGGAGCAG 453  
 QY 421 GTTTCATTTTTCGAGGAGAGCGGAGCATATATTATCTC 457  
 Db 454 GTTTCATTTTTCGAGGAGAGGAGCAATATTATCCC 490

RESULT 9  
 BI654262 821 bp mRNA linear EST 12-SEP-2001  
 LOCUS 603280370F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:5310496 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI654262  
 VERSION BI654262  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLNL1786 row: 1 column: 17  
 High quality sequence stop: 648.

## FEATURES

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 Location/Qualifiers  
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 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
 /clone="IMAGE:5310496"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Mam4"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Priscilla Furth,  
 NIH Reference for transgenic model: Li et al., Cell Growth  
 and Differentiation 7, 3-11 (1996)."

## ORIGIN

Query Match 22.7%; Score 344.2; DB 4; Length 821;  
 Best Local Similarity 84.5%; Pred. No. 3.4e-93;  
 Matches 469; Conservative 0; Mismatches 78; Indels 8; Gaps 7;  
 QY 1 GGGGAGATGTTGAAGTTCAATATGGAGCGCGAATCTTTGGATCGTGGTCTGTA 60  
 Db 101 GGAGAGATGTTGAAGTTCAAGTGTGTGCGAACCCTCCGAGGCCAGTGCCTCCGAG 160  
 QY 61 CCATTGCCAACCGGGCTCCAGGCTGAATCTTTTTCAGGGGAAACACCTTTATG 120  
 Db 161 CCATTGCCAGTCGGGCTCCAGGCTAAATCTTCTTCAGGGGAAACCGGCTCATG 220  
 QY 121 ACTCAACAGCAGATGCTCTCTTTCCCGAGAGGGATATTAGATCCCTCTTTGTC 180  
 Db 221 ACTCAACAGCAGATGCTCTCTTTCCCGAGAGGGATAGTACGCCCTCTTCGCTCTC 280

QY 181 TTTGAAGATGCACTCAGCTCAGCTGCTCTGATGAAGATTAAGCACGCTGAGCAACTTTTGCCGG 240  
 Db 281 TTGGAAGAGTGCAGCCCAACCCGCCCTGATGAAGATGAAGCACGCTGAGCAGCTTAGTCCAG 340  
 QY 241 AAGTATTTCCGACACCATAG-CTGAGTTACAGGAGCTCCAGCCTTCGCAAGAGCACTTCGA 299  
 Db 341 AAGTATTTCCGACACCATAGCCCGAGTTGCGGGAGCTGCAGCCGCTCGCGGAGAGACTTCGA 400  
 QY 300 A-GTCAGAAGTCTTTGTAGTTTGGTTCACCTTTGCTGAAGTGCAGGTGG-TAAGAGAGAAA 357  
 Db 401 AGTTCCGAAGCCTTGTGGCTGTGGTCACTTCGCTGAAGTGCAGGTGGTACGAGAGAAG 460  
 QY 358 GCAACCCGGGACACTATGCTATGATAAAGTGATGA-AGAAGAAGCTTTATTGGCCCGAGGA 416  
 Db 461 GCGACCCGGGACGCTATATGTCATGAAATCATGACAGAGAAGGCTTTTGTGCCCCAGGA 520  
 QY 417 GCAGGTTTCATTTTTCGAGGAAGAGCGGAA-CATATTATCTCGAAGCACAGGCCGCTGGA 475  
 Db 521 ACAGTTTTCATTTTTCGAGGAGGAGGAACCAATATATCTCGAGGACGAGTCTTGA 580  
 QY 476 TCCCCCAATTACAGTATGCTTTTCAGGA-CAAAAATACCTTTATCTGTCGTCATGG--AAT 532  
 Db 581 TCCACCAAGTTACAGTACGCTTTTCAGGACCAAAAATAAACTTTTACCTGGTCATGGACACT 640  
 QY 533 ATCAGCCTGGAGGG 547  
 Db 641 ATCAGCCTGGATGG 655

## RESULT 10

CG501400 450 bp DNA linear GSS 01-OCT-2003  
 LOCUS OST45250 Mus musculus 129Sv/Ev Mus musculus genomic clone OST45250,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG501400  
 VERSION CG501400.1 GI:37275069  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 450)  
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,  
 Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,  
 Fridele,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,  
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,  
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,  
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,  
 Zhu,Q., Person,C. and Sands,A.T.  
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)  
 Contact: Zambrowicz BP  
 OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: [materials@lexgen.com](mailto:materials@lexgen.com)  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene trap.  
 Location/Qualifiers  
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 /db\_xref="taxon:10090"  
 /clone="OST45250"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## FEATURES

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 /mol\_type="genomic DNA"  
 /strain="129Sv/Ev"  
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 /clone\_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 21.7%; Score 329.2; DB 9; Length 450;  
 Best Local Similarity 90.0%; Pred. No. 1e-88;



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Query Match		21.0%; Score 318.2; DB 9; Length 512;	
Best Local Similarity		92.0%; Pred. No. 2.5e-85;	
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QY	1118	CTCCTCCCCCTTCGTTCCACCTCAAGTCCAGCATGACACCTCCAAATTTTGATGAAC	1177
DB	6	CTCCTCCCCCTTCGTTCCACCTCAAGTCCAGCATGACACCTCCAAATTTTGATGAAC	65
QY	1178	CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGAGCTGAGCCCTCAGGCTTCTCGG	1237
DB	66	CAGAGAAGAAATTCGTGGGTTTCATCTCTCTGTCGACAGTGGCCCTCGGCTTCTAG	125
QY	1238	GTGAAGAACTGCGGTTTGTGGGTTTTCGTTACAGCAAGCACTGCGGATCTCTGGTAGAT	1297
DB	126	GCGAAGAACTGCGGTTTGTGGGTTTTCGTTACAGCAAGCACTGCGGATCTCTGGTAGAT	185
QY	1298	CTGAGTCTGTGTCGGGTTTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	1357
DB	186	CTGAGTCTGTGTCGGGTTTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	245
QY	1358	TTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTT	1417
DB	246	TTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTT	305
QY	1418	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	1477
DB	306	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	1477
QY	1478	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	1493
DB	366	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	381
RESULT 13		512 bp DNA linear GSS 02-OCT-2003	
CG652891		OST417039 Mus musculus 129Sv/Ev Mus musculus genomic clone	
LOCUS		OST417039, genomic survey sequence.	
ACCESSION		CG652891	
VERSION		GSS.	
KEYWORDS		Mus musculus (house mouse)	
SOURCE		Mus musculus	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS		Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., Beirand, R.H., Buxton, E.C., Edwards, J., Finch, R.A., Fiddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaling, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.	
TITLE		Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)	
COMMENT		Contact: Zambrowicz BP OmniBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap. Location/Qualifiers 1. .512 /organism="Mus musculus" /mol_type="genomic DNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OST417039"	
FEATURES		source	
ORIGIN		Query Match	
		Best Local Similarity	
		Matches 346; Conservative	
		0; Mismatches 29; Indels 1; Gaps 1;	
QY	1118	CTCCTCCCCCTTCGTTCCACCTCAAGTCCAGCATGACACCTCCAAATTTTGATGAAC	1177
DB	8	CTCCTCCCCCTTCG-TCCCCCCTCAAGTCTGACGATGACACCTCCAAATTTTGATGAAC	66
QY	1178	CAGAGAAGAAATTCGTGGGTTTCATCTCTCCGTCGAGCTGAGCCCTCAGGCTTCTCGG	1237
DB	67	CAGAGAAGAAATTCGTGGGTTTCATCTCTCTGTCGACAGTGGCCCTCGGCTTCTAG	126
QY	1238	GTGAAGAACTGCGGTTTGTGGGTTTTCGTTACAGCAAGCACTGCGGATCTCTGGTAGAT	1297
DB	127	GCGAAGAACTGCGGTTTGTGGGTTTTCGTTACAGCAAGCACTGCGGATCTCTGGTAGAT	186
QY	1298	CTGAGTCTGTGTCGGGTTTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	1357
DB	187	CTGAGTCTGTGTCGGGTTTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAAAC	246
QY	1358	TTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTT	1417
DB	247	TTCTCATCAAAAGCAAGAGCTCAAGACTCTCAGGACAAAGTGTCAAGAGTATTTATTT	306
QY	1418	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAGATCCG	1477
DB	307	CCACAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAGATCCG	366
QY	1478	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAGATCCG	1493
DB	367	CCGAGCGGCTCTCTCTGTCGAGTCTCCCTCCCAAGTCTCCATGCGAAGAGATCCG	382
RESULT 14		340 bp mRNA linear EST 27-NOV-2000	
BF380737		IL2-UT0073-170900-167-H01 UT0073 Homo sapiens cDNA, mRNA sequence.	
LOCUS		BF380737	
DEFINITION		BF380737	
ACCESSION		BF380737.1	
VERSION		GI:11369862	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and Simpson, A.J.	
TITLE		Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
COMMENT		Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-UT0073- 170900-167-H01&t3=2000-09-17&t4=1) Seq primer: puc 18 forward	

